ACACCAATCCAAAAGCGTGGAACTATGTTAAAAAGCTACAACATAATATT
AATGCTATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGA
AGGAAAAATGATTGTGGGGTTGACTTACGAAGACCCTAGTGTCAATTTGC
AAAAAAGTGGTGCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTT
TTTGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGA
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TTGGGCAGTCAACGAGTAACCGACCTATTCGTAAAGATGCCCAAACGAGT
AATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCG
CTATGTCACTAAGCATAAGGGCCAAATCCTTAAAACCTATAATCGTATTC
GTAGAAATGCTGAT

SEQ ID NO. 6004
STRAIN H36B
TAAACTACTTCCACCAAAAGAATTAGTTATTCTAAGTCCAAATAGTCAAG
CCATTTTAACAGGAACGATTCCAGCTTTTGAGGAAAAATACGGTATAAAA
GTTAAGCTTATTCAAGGTGGGACAGGTCAACTAATAGATAGATTAAGTAA
GGAGGGTAAGCAGTTGAAGGCGGATATTTTCTTTGGAGGAAATTATACGC
AATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAAAGAATATT
CATACTGTTATTCCAGATTATATCCATCCGAGTGATACGGCGACACCTTA
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TTACCATCAAGAGTTATGAAGATTTATTACAGCCTTCCTTAAAAGGTAAA
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TAATATACTCTTGGCCAAGGGTGGTTACACCAATCCAAAAGCGTGGAACT
ATGTTAAAAAGCTACAACATAATATTAATGCTATCAAATCTTCTAGCTCT
TCAGAAGTTTATCAATCAGTTGCAGAAGGAAAAATGATTGTGGGGTTGAC
TTACGAAGACCCTAGTGTCAATTTGCAAAAAAGTGGTGCCAATGTTTCTA
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GCTTTCTTTAGATGTTCAAAATGCCTTTGGGCAGTCAACGAGTAACCGAC
CTATTCGTAAAGATGCCCAAACGAGTAATGGCATGAAAGCTTTAAAGGAT
ATTGCTACTCTTAAAGAAGATTATCGCTATGTCACTAAGCATAAGGGCCA
AATCCTTAAAACCTATAATCGTATTCGTAGAAATGCTGAT

SEQ ID NO. 6005
STRAIN 18RS21
CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGTTATTCTAAGTCCAAA
TAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTTTGAGGAAAAATACG
GTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAGA
TTAAGTAAGGAGGGTAAGCAGTTGAAGGCGgATATTTTCTTTGGAGGAAA
TTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAA
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ACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAATAACGAATTAGC
TAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGCCTTCCTTAA
AAGGTAAAATTGCCTTTGCAGATCCGAATACTTCCTCTAGTGCTTTCTCA
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TTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTTATT
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TAACCGACCTATTCGTAAAGATGCCCAAACGAGTAATGGCATGAAAGCTT
TAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTCACTAAGCAT
AAGGGCCAAATCCTTAAAACCTATAATCGTATTCGTAGAAATGCTGAT

SEQ ID NO. 6006
STRAIN M732
CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGT
TATTCTAAGTCCAAATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTT
TTGAGGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGG
CAACTAATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATAT
TTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTG
AGTCTTACGTATCAAAGAATGTTCATACTGTTATTCCAGACTATATCCAT
CCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGT

SEQUENCE LISTING

AAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTAT
TACAGCCTTCCTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCC
TCTAGTGCTTTCTCACAACTCACTAATATACTCTTGGCCAAGGGTGGTTA
CACCAATCCAAAAGCGTGGAACTATGTTAAAAAGCTACAACATAATATTA
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AAAAAGTGGTGCCAATGTTTCTATTGTATACCCGACAGAAGGGACAGTTT
TTGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAA
GCAAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTT
TGGGCAGTCAACGAGTAACCGACCTATTCGTAAAGATGCCCAAACAAGTA
ATGGCATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGC
TATGTCACTAAGCATAAGAGCCAAATCCTTAAAACCTATAATCGCATTCG
TAGAAATGCTGAT

SEQ ID NO. 6007
STRAIN COH1
CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGTT
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TGAGGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGC
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TTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGA
GTCTTACGTATCAAAGAATGTTCATACTGTTATTCCAGACTATATCCATC
CGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTA
AATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATT
ACAGCCTTCCTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCCT
CTAGTGCTTTCTCACAACTCACTAATATACTCTTGGCCAAGGGTGGTTAC
ACCAATCCAAAAGCGTGGAACTATGTTAAAAAGCTACAACATAATATTAA
TGCTATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAG
GAAAAATGATTGTGGGGTTGACTTACGAAGACCCTAGTGTCAATTTGCAA
AAAGTGGTGCCAATGTTTCTATTGTATACCCGACAGAAGGGACAGTTTT
TGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAG
CAAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTTT
GGGCAGTCAACGAGTAACCGACCTATTCGTAAAGATGCCCAAACAAGTAA
TGGCATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCT
ATGTCACTAAGCATAAGAGCCAAATCCTTAAAACCTATAATCGCATTCGT
AGAAATGCTGAT

SEQ ID NO. 6008
STRAIN M781
CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGTTATT
CTAAGTCCAAATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTTTGA
GGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAAC
TAATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTTC
TTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTC
TTACGTATCAAAGAATGTTCATACTGTTATTCCAGACTATATCCATCCGA
GTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAAT
AACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACA
GCCTTCCTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCCTCTA
GTGCTTTCTCACAACTCACTAATATACTCTTGGCCAAGGGTGGTTACACC
AATCCAAAAGCGTGGAACTATGTTAAAAAGCTACAACATAATATTAATGC
TATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAGGAA
AAATGATTGTGGGGTTGACTTACGAAGACCCTAGTGTCAATTTGCAAAAA
AGTGGTGCCAATGTTTCTATTGTATACCCGACAGAAGGGACAGTTTTTGT
CCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAA
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CAGTCAACGAGTAACCGACCTATTCGTAAAGATGCCCAAACAAGTAATGG
CATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCTATG
TCACTAAGCATAAGAGCCAAATCCTTAAAACCTATAATCGCATTCGTAGA
AATGCTGAT

SEQ ID NO. 6009
STRAIN CJB110
CAGCCTTTTAAACTACTTCCACCAAAAGAATTAGTTATTCT
AAGTCCAAATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTTTGAGg

AAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTA
ATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTTCTT
TGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTT
ACGTATCAAAGAATGTTCATACTGTTATTCCAGACTATATCCATCCAAGT
GATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAATAA
CGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGC
CTTCCTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCCTCTAGT
GCTTTCTCACAACTCACTAATATACTCTTGGCCAAGGGTGGTTACACCAA
TCCAAAAGCGTGGAACTATGTTAAAAAGCTACAACATAATATTAATGCTA
TCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAGGAAAA
ATGATTGTGGGGCTGACTTACGAAGACCCTAGTGTCAATTTGCAAAAAAG
TGGTGCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTTTGTCC
CATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAG
TTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGGCA
GTCAACGAGTAACCGACCTATTCGTAAAGATGCCCAAACGAGTAATGGCA
TGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTC
ACTAAGCATAAGGGCCAAATCCTTAAAACCTATAATCGTATTCGTAGAAA
TGCTGAT

SEQ ID NO. 6010
STRAIN 1169NT
ATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTTTGAGGAAAAATAC
GGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAG
ATTAAGTAAGGAGGGTAAGCATTTGAAGGCGGATATTTTCTtTGGAGGAA
ATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCA
AAGAATGTTCATACTGTTATTCCAGACTATATCCATCCAAGTGATACGGC
GACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAATAACGAATTAG
CTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGCCTTCCTTA
AAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCCTCTAGTGCTTTCTC
ACAACTCACCAATATACTCTTGGCAAAGGGTGGTTACACCAATCCAAAAG
CGTGGAACTATGTTAAAAAGCTACAACATAATATTAATGCTATCAAATCT
TCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAGGAAAAATGATTGT
GGGGTTGACTTACGAAGACCCTAGTGTCAATTtGCAAAAAAGTGGTGCCA
ATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTTTGTCCCATCTTCG
GTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTTAT
TAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGGCAGTCAACGA
GTAACCGACCTATTCGTAAAGATGCCCAAACGAGTAATGGCATGAAAGCT
TTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTCACTAAGCA
TAAGGGCCAAATCCTTAAAACCTATAATCGTATTCGTAGAAATGCTGAT

SEQ ID NO. 6011
STRAIN JM91130013
CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGT
TATTCTAAGTCCAAATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTT
TTGAGGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGG
CAACTAATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATGT
TTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTG
AGTCTTACGTATCAAAGAATGTTCATACTGTTATTCCAGACTATATCCAT
CCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGT
AAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTAT
TACAGCCTTCCTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCC
TCTAGTGCTTTCTCACAACTCACCAATATACTCTTGGCAAAGGGTGGTTA
CACCAATCCAAAAGCGTGGAACTATGTTAAAAAGCTACAACATAATATTA
ATGCTATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAA
GGCAAAATGATTGTGGGGCTGACTTACGAAGACCCTAGTGTCAATTTGCA
AAAAAGTGGTGCCAATGTTTCTATTGTGTATCCGACAGAAGGGACAGTTT
TTGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAA
GCAAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTT
TGGGCAGTCAACGAGTAACCGACCTATTCGTAAAGATGCCCAAACGAGTA
ATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGC
TATGTCACTAAGCATAAGGGCCAAATCCTTAAAACCTATAATCGTATTCG
TAGAAATGCTGAT

SEQ ID NO. 6012

SEQUENCE LISTING

STRAIN 2603 frame: 1
MKEKQSKRLIYILLVVSIIFISVFTYSISQPSKLLPPKELVILSPNSQAILTGTIPAFEE
KYGIKVKLIQGGTGQLIDRLSKEGKQLKADIFFGGNYTQFESHKALFESYVSKNVHTVIP
DYIHPSDTATPYTINGSVLIVNNELAKGLTIKSYEDLLQPSLKGKIAFADPNTSSSAFSQ
LTNILLAKGGYTNPKAWNYVKKLQHNINAIKSSSSSEVYQSVAEGKMIVGLTYEDPSVNL
QKSGANVSIVYPTEGTVFVPSSVAIIKNAPSMKEAKLFINFMLSLDVQNAFGQSTSNRPI
RKDAQTSNGMKALKDIATLKEDYRYVTKHKGQILKTYNRIRRNAD

SEQ ID NO. 6013
STRAIN 090 frame: 1
QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KGQILKTYNRIRRNAD

SEQ ID NO. 6014
STRAIN A909 frame: 1
QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNIHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KGQILKTYNRIRRNAD

SEQ ID NO. 6015
STRAIN H36B frame: 2
KLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKADIF
FGGNYTQFESHKALFESYVSKNIHTVIPDYIHPSDTATPYTINGSVLIVNNELVKGLTIK
SYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINAIKS
SSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNAPSM
KEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKHKGQ
ILKTYNRIRRNAD

SEQ ID NO. 6016
STRAIN 18RS21 frame: 1
QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KGQILKTYNRIRRNAD

SEQ ID NO. 6017
STRAIN M732 frame: 1
QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KSQILKTYNRIRRNAD

SEQ ID NO. 6018
STRAIN COH1 frame: 1
QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KSQILKTYNRIRRNAD

SEQ ID NO. 6019
STRAIN M781 frame: 1

SEQUENCE LISTING

QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KSQILKTYNRIRRNAD

SEQ ID NO. 6020
STRAIN CJB110 frame: 1
QPFKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KGQILKTYNRIRRNAD

SEQ ID NO. 6021
STRAIN 1169NT frame: 3
SQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKHLKADIFFGGNYTQFESHKAL
FESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGLTIKSYEDLLQPSLKGKI
AFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINAIKSSSSSEVYQSVAEGK
MIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNAPSMKEAKLFINFMLSLD
VQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKHKGQILKTYNRIRRNAD

SEQ ID NO. 6022
STRAIN JM91130013 frame: 1
QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DVFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KGQILKTYNRIRRNAD

SEQ ID NO. 6101
STRAIN 2603
ATGGTAAAAGTTAGTGTAAGTTCTGTAGGAACTCAAGCATCAACAGTAGCTATTTCTATG
TTTAGTCGTGTATCGGCTTTAAATGATGCAATAACAAAACTATCATCTTTTGCAGAGGCT
GCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGGAACGTTAACT
CCGATGCTTCAAGGAATGATTCTTTTCTCTGAAACATTGAGTGAGAAATGTACAGAATTA
CAAACCTTATATGTCTCAATTTGTGGTGATGAGGATTTAGACTCTGTCGTTTTAGAATCA
AAATTAGCAAGTGATAGGGCATCATTAAAGATTGCTGAAGCACTTTTAGAGCATCTTAAC
GATGATCCAGAACCTTCCAAATCTGCCATAAGTTCTACAAAAAGTAATATTAAAAAATTA
AAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAATTTAACGCCCAT
TCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAACTGTTAACCAAGCACTAGCG
GCTGTTTCAACAGGATTTTCTGGATATAATAGTAAAACCGGAGCTTTTGGAAAACCAACA
TCCGGACAGATGGAATGGACAAAGACAGTTAAGAAGAATTGGAAAGAGCGAGAAGACGCC
AAAGCTGAAGAACTGAAAAGTAAAAAGGCTGAAGAAAGTAAGAAAGCTTCAAAAATTGAA
AATACTACTAAAAAAAGTAATGTTTCAGTTGATAAAAAGAAATTAATAAAAGCGGCTAAT
GAAGCGTATAAATTAGGAGAAATTAAAAAAGATACCTATGAATCAATTATCAGTGGTTTA
AGTAATGCATCGGCTGCCTTACTTAAAGAGGTAGCTAAATCAAAATTGACTGACACAGCT
CGGCTATTGATG

SEQ ID NO. 6102
STRAIN 090
TTAAATGATGCAATAACAAAACTATCATCTTTTGCAGAGGCT
GCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGG
AACGTTAACTCCGATGCTTCAAGGAATGATTCTTTTCTCTGAAACATTGA
GTGAGAAATGTACAGAATTACAAACCTTATATGTCTCAATTTGTGGTGAT
GAGGATTTAGACTCTGTCGTTTTAGAATCAAAATTAGCAAGTGATAGGGC
ATCATTAAAGATTGCTGAAGCACTTTTAGAGCATCTTAACGATGATCCAG
AACCTTCCAAATCTGCCATAAGTTCTACAAAAAGTAATATTAAAAAATTA
AAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAATT
TAACGCCCATTCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAA
CTGTTAACCAAGCACTAGCGGCTGTTTCAACAGGATTTTCTGGATATAAT

SEQUENCE LISTING

AGTAAAACCGGAGCTTTTGGAAAACCAACATCCGGACAGATGGAATGGAC
AAAGACAGTTAAGAAGAATTGGAAAGAGCGAGAAGACGCCAAAGCTGAAG
AACTGAAAAGTAAAAAGGCTGAAGAAAGTAAGAAAGCTTCAAAAATTGAA
AATACTACTAAAAAAAGTAATGTTTCAGTTGATAAAAAGAAATTAATAAA
AGCGGCTAATGAAGCGTATAAATTAGGAGAAATTAAAAAAGATACCTATG
AATCAATTATCAGTGGTTTAAGTAATGCATCGGCTGCCTTACTTAAAGAG
GTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

SEQ ID NO. 6103
STRAIN 18RS21
TTAAATGATGCAATAACAAAACTATCATCTTTTGCAGAGGC
TGCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTG
GAACGTTAACTCCGATGCTTCAAGGAATGATTCTTTTCTCTGAAACATTG
AGTGAGAAATGTACAGAATTACAAACCTTATATGTCTCAATTTGTGGTGA
TGAGGATTTAGACTCTGTCGTTTTAGAATCAAAATTAGCAAGTGATAGGG
CATCATTAAAGATTGCTGAAGCACTTTTAGAGCATCTTAACGATGATCCA
GAACCTTCCAAATCTGCCATAAGTTCTACAAAAAGTAATATTAAAAAATT
AAAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAAT
TTAACGCCCATTCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCA
ACTGTTAACCAAGCACTAGCGGCTGTTTCAACAGGATTTTCTGGATATAA
TAGTAAAACCGGAGCTTTTGGAAAACCAACATCCGGACAGATGGAATGGA
CAAAGACAGTTAAGAAGAATTGGAAAGAGCGAGAAGACGCCAAAGCTGAA
GAACTGAAAAGTAAAAAGGCTGAAGAAAGTAAGAAAGCTTCAAAAATTGA
AAATACTACTAAAAAAAGTAATGTTTCAGTTGATAAAAAGAAATTAATAA
AAGCGGCTAATGAAGCGTATAAATTAGGAGAAATTAAAAAAGATACCTAT
GAATCAATTATCAGTGGTTTAAGTAATGCATCGGCTGCCTTACTTAAAGA
GGTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

SEQ ID NO. 6104
STRAIN 2603 frame: 1
MVKVSVSSVGTQASTVAISMFSRVSALNDAITKLSSFAEAATLQGTAYSNAKSYATGTLT
PMLQGMILFSETLSEKCTELQTLYVSICGDEDLDSVVLESKLASDRASLKIAEALLEHLN
DDPEPSKSAISSTKSNIKKLKKRIKSNQKKLDNLNEFNAHSATVFADISNAQSTVNQALA
AVSTGFSGYNSKTGAFGKPTSGQMEWTKTVKKNWKEREDAKAEELKSKKAEESKKASKIE
NTTKKSNVSVDKKKLIKAANEAYKLGEIKKDTYESIISGLSNASAALLKEVAKSKLTDTA
RLLM

SEQ ID NO. 6105
STRAIN 090 frame: 1
LNDAITKLSSFAEAATLQGTAYSNAKSYATGTLTPMLQGMILFSETLSEKCTELQTLYVS
ICGDEDLDSVVLESKLASDRASLKIAEALLEHLNDDPEPSKSAISSTKSNIKKLKKRIKS
NQKKLDNLNEFNAHSATVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEW
TKTVKKNWKEREDAKAEELKSKKAEESKKASKIENTTKKSNVSVDKKKLIKAANEAYKLG
EIKKDTYESIISGLSNASAALLKEVAKSKLTDTARLLM

SEQ ID NO. 6106
STRAIN 18RS21 frame: 1
LNDAITKLSSFAEAATLQGTAYSNAKSYATGTLTPMLQGMILFSETLSEKCTELQTLYVS
ICGDEDLDSVVLESKLASDRASLKIAEALLEHLNDDPEPSKSAISSTKSNIKKLKKRIKS
NQKKLDNLNEFNAHSATVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEW
TKTVKKNWKEREDAKAEELKSKKAEESKKASKIENTTKKSNVSVDKKKLIKAANEAYKLG
EIKKDTYESIISGLSNASAALLKEVAKSKLTDTARLLM

SEQ ID NO. 6201
STRAIN 2603
ATGATTTTAAAAATTTGTCGTGCAGCATATAGTTTACAATGGGGAGGTGTTTACCAATTA
GCTTTGCTGGATTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATA
GCTTACGAGAAACAATATAAAAGAAAAACTGAGATACAATGTGACGATAAACATCTCCTC
GCAAAAATTGTTCATTTTTTAAAATACAATAGTTTTACTTTTCCCTATATTCCCAAATAT
AGAGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTAACTTCTGATTTTTTAAGC
CATACATGTACGATTGAAACTGCAAAACTAATTTTTAAAGAAGGTAAAATCTTATCAGCA
GTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGA
GACCCTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTAT
CGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGT

TTTAAGCCAGGGGTCAGTTTTCATTTTACTTATCAAGATATCATCAATCATCCTGATTCT
ATTTTTGATGGTTATCATCCTGCTAAAATTAAAAATCAGCTTTCTTTAGCAGAACATTTA
GTTGCATGTGTTATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGAC
TTGAAACACAGGGTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAA
AAAGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6202
STRAIN 090
TGGATTATCCTCTAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTC
ATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGATACAATGTGACGA
TAAACATCTCCTCACAAAAATTGTTCATTTTTTAAAATACAATAGTTTTA
CTTTTCCCTATATTCCCAAATATAGAGAAGCGGCAGCTACTTTTAATGAG
GATGGTATTAGTTTAACTTCTGATTTTTTAAGCCATACATGTACGATTGA
AACTGCAAAACTAATTTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAG
CCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCT
GGAGACCCTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATAC
CAATTCTGGTTATCGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCAT
CTGAACAGGAGTTAACAGTAGCTTTTAAGCCAGGGGTCAGCTTTCATTTT
AATTaTCAAGATATCATCAATCATCCTGATTCTATTTTTGATGGTTATCA
TCCTGCTAAAATTAAAAATCAACTTTCTTTAGCAGAACATTTAGTTGCAT
GTGTTATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCTAAT
GACTTGAAACACAGAGTTTATTATTTAGATTACTGTAACGAAACACTTTA
TGAGTGGAATCAAAAAGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6203
STRAIN A909
TTGCTGGATTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATA
GGAGCTTTCATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGATACA
ATGTGACGATAAACATCTCCTCACAAAAATTGTTCATTTTTTAAAATACA
ATAGTTTTACTTTTCCCTATATTCCCAAATATAGAGAAGCGGCAGCTACT
TTTAATGAGGATGGTATTAGTTTAACTTCTGATTTTTTAAGCCATACATG
TACGATTGAAACTGCAAAACTAATTTTTAAAGAAGGTAAAATCTTATCAG
CAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAGAGG
AATGCTGCTGGAGACCCTAAAGATTACTTTGACTATGTGATGTTGAACTG
GTCAAATACCAATTCTGGTTATCGTTTAGTAATGGAAAGATTGTTAGGCA
AAGCACCATCTGAACAGGAGTTAACAGTAGCTTTTAAGCCAGGGGTCAGC
TTTCATTTTAATTATCAAGATATCATCAATCATCCTGATTCTATTTTTGA
TGGTTATCATCCTGCTAAAATTAAAAATCAACTTTCTTTAGCAGAACATT
TAGTTGCATGTGTTATCCCAAAACATTATCAAGAAGATTATCAAAGCCTT
GTGCCTAATGACTTGAAACACAGAGTTTATTATTTAGATTACTGTAACGA
AACACTTTATGAGTGGAATCAAAAAGTTTATGATTTTCTTTGTCATTTGG
AAAATAAA

SEQ ID NO. 6204
STRAIN H36B
TTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAA
CAATATAAAAGAAAAATTGAGATACAATGTGACGATAAACATCTCCTCAC
AAAAATTGTTCATTTTTTAAAATACAATAGTTTTACTTTTCCCTATATTC
CCAAATATAGAGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTA
ACTTCTGATTTTTTAAGCCATACATGTACGATTGAAACTGCAAAACTAAT
TTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTG
CTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCTAAAGAT
TACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCG
TTTAGTAATGGAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAA
CAGTAGCTTTTAAGCCAGGGGTCAGCTTTCATTTTAATTATCAAGATATC
ATCAATCATCCTGATTCTATTTTTGATGGTTATCATCCTGCTAAAATTAA
AAATCAACTTTCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAAAC
ATTATCAAGAAGATTATCAAAGCCTTGTGCCTAATGACTTGAAACACAGA
GTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAA
AGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6205
STRAIN 18RS21
TTGCTGGATTATCCTCGAATTAAGGCGTT

TGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAA
GAAAAACTGAGATACAATGTGACGATAAACATCTCCTCGCAAAAATTGTT
CATTTTTTAAAATACAATAGTTTTACTTTTCCCTATATTCCCAAATATAG
AGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTAACTTCTGATT
TTTTAAGCCATACATGTACGATTGAAACTGCAAAACTAATTTTTAAAGAA
GGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACT
GGTAAAAGATAAGAGGAATGCTGCTGGAGACCCTAAAGATTACTTTGACT
ATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCGTTTAGTAATG
GAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGTTT
TAAGCCAGGGGTCAGTTTTCATTTTACTTATCAAGATATCATCAATCATC
CTGATTCTATTTTTGATGGTTATCATCCTGCTAAAATTAAAAATCAGCTT
TCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAAACATTATCAAGA
AGATTATCAAAGCCTTGTGCCCAATGACTTGAAACACAGGGTTTATTATT
TAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAAAGTTTATGAT
TTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6206
STRAIN M732
TTGCTGGATTATCCTCGAATTAAGGCGTT
TGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAA
GAAAAACTGAGATACAATGTGACGATAAACATCTCCTCGCAAAAATTGTT
CATTTTTTAAAATACAATAGTTTTACTTTTCCCTATATTCCCAAATATAG
AGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTAACTTCTGATT
TTTTAAGCCATACATGTACGATTGAAACTGCAAAACTAATTTTTAAAGAA
GGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACT
GGTAAAAGATAAGAGGAATGCTGCTGGAGACCCTAAAGATTACTTTGACT
ATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCGTTTAGTAATG
GAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGTTT
TAAGCCAGGGGTCAGTTTTCATTTTACTTATCAAGATATCATCAATCATC
CTGATTCTATTTTTGATGGTTATCATCCTGCTAAAATTAAAAATCAGCTT
TCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAAACATTATCAAGA
AGATTATCAAAGCCTTGTGCCCAATGACTTGAAACACAGGGTTTATTATT
TAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAAAGTTTATGAT
TTTCTTTGnCATTTGGAAAATAAA

SEQ ID NO. 6207
STRAIN COH1
TTGCTGGAT
TATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGC
TTACGAGAAACAATATAAAAGAAAAACTGAGATACAATGTGACGATAAAC
ATCTCCTCGCAAAAATTGTTCATTTTTTAAAATACAATAGTTTTACTTTT
CCCTATATTCCCAAATATAGAGAAGCGGCAGCTACTTTTAATGAGGATGG
TATTAGTTTAACTTCTGATTTTTTAAGCCATACATGTACGATTGAAACTG
CAAAACTAATTTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTTT
AATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGAGA
CCCTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATT
CTGGTTATCGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCATCTGAA
CAGGAGTTAACAGTAGGTTTTAAGCCAGGGGTCAGTTTTCATTTTACTTA
TCAAGATATCATCAATCATCCTGATTCTATTTTTGATGGTTATCATCCTG
CTAAAATTAAAAATCAGCTTTCTTTAGCAGAACATTTAGTTGCATGTGTT
ATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGACTT
GAAACACAGGGTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGT
GGAATCAAAAAGTTTATGATTTTCTTTGGCATTTGGAAAATAAA

SEQ ID NO. 6208
STRAIN M781
TTGCTGGA
TTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAG
CTTACGAGAAACAATATAAAAGAAAAACTGAGATACAATGTGACGATAAA
CATCTCCTCGCAAAAATTGTTCATTTTTTAAAATACAATAGTTTTACTTT
TCCCTATATTCCCAAATATAGAGAAGCGGCAGCTACTTTTAATGAGGATG
GTATTAGTTTAACTTCTGATTTTTTAAGCCATACATGTACGATTGAAACT
GCAAAACTAATTTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTT
TAATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGAG

SEQUENCE LISTING

ACCCTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAAT
TCTGGTTATCGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCATCTGA
ACAGGAGTTAACAGTAGGTTTTAAGCCAGGGGTCAGTTTTCATTTTACTT
ATCAAGATATCATCAATCATCCTGATTCTATTTTTGATGGTTATCATCCT
GCTAAAATTAAAAATCAGCTTTCTTTAGCAGAACATTTAGTTGCATGTGT
TATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGACT
TGAAACACAGGGTTTATTATTTAGATTACTGTAACGAAACACTTTATGAG
TGGAATCAAAAAGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6209
STRAIN CJB110
TTGCTGGATTATCCTCGAATTAAGGC
GTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATA
AAAGAAAAATTGAGATACAATGTGACGATAAACATCTCCTCACAAAAATT
GTTCATTTTTTAAAATACAATAGTTTTACTTTTCCCTATATTCCCAAATA
TAGAGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTAACTTCTG
ATTTTTTAAGCCATACATGTACGATTGAAACTGCAAAACTAATTTTTAAA
GAAGGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGT
ACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCTAAAGATTACTTTG
ACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCGTTTAGTA
ATGGAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGC
TTTTAAGCCAGGGGTCAGCTTTCATTTTAATTATCAAGATATCATCAATC
ATCCTGATTCTATTTTTGATGGTTATCATCCTGCTAAAATTAAAAATCAA
CTTTCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAAACATTATCA
AGAAGATTATCAAAGCCTTGTGCCTAATGACTTGAAACACAGAGTTTATT
ATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAAAGTTTAT
GATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6210
STRAIN 1169NT
AATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGA
AACAATATAAAAGAAAAACTGAGATACAATGTGACGATAAACATCTCCTC
GCAAAAATTGTTCATTTTTTAAAATACAATAGTTTTACTTTTCCCTATAT
TCCCAAATATAGAGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTT
TAACTTCTGATTTTTTAAGCCATACATGTACGATTGAAACTGCAAAACTA
ATTTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCC
TGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCTAAAG
ATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTAT
CGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTT
AACAGTAGGTTTTAAGCCAGGGGTCAGCTTTCATTTTACTTATCAAGATA
TCATCAATCATCCTGATTCTATTTTTGATGGTTATCATCCTGCTAAAATT
AAAAATCAGCTTTCTTTAGCAGAACATTTAGTTGCGTGTGTTATCCCAAA
ACATTATCAAGAAGATTATCAAAATCTTGTGCCCAATGACTTGAAACACA
GAGTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAA
AAAGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6211
STRAIN JM9130013
ATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGAT
ACAATGTGACGATAAACATCTCCTCACAAAAATTGTTCATTTTTTAAAAT
ACAATAGTTTTACTTTTCCCTATATTCCCAAATATAGAGAAGCGGCAGCT
ACTTTTAATGAGGATGGTATTAGTTTAACTTCTGATTTTTTAAGCCATAC
ATGTACGATTGAAACTGCAAAACTAATTTTTAAAGAAGGTAAAATCTTAT
CAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAG
AGGAATGCTGCTGGAGACCCTAAAGATTACTTTGACTATGTGATGTTGAA
CTGGTCAAATACCAATTCTGGTTATCGTTTAGTAATGGAAAGATTGTTAG
GCAAAGCACCATCTGaACAGGAGTTAACAGTAGCTTTTAAGCCAGGGGTC
AGCTTTCATTTTAATTATCAAGATATCATCAATCATCCTGATTCTATTTT
TGATGGTTATCATCCTGCTAAAATTAAAAATCAACTTTCTTTAGCAGAAC
ATTTAGTTGCATGTGTTATCCCAAAACATTATCAAGAAGATTATCAAAGC
CTTGTGCCTAATGACTTGAAACACAGAGTTTATTATTTAGATTACTGTAA
CGAAACACTTTATGAGTGGAATCAAAAAGTTTATGATTTTCTTTGTCATT
TGGAAAATAAA

SEQUENCE LISTING

SEQ ID NO. 6212
STRAIN 2603 frame: 1
MILKICRAAYSLQWGGVYQLALLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLL
AKIVHFLKYNSFTFPYIPKYREAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSA
VKAFNKPAEVLVKDKRNAAGDPKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVG
FKPGVSFHFTYQDIINHPDSIFDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPND
LKHRVYYLDYCNETLYEWNQKVYDFLCHLENK

SEQ ID NO. 6213
STRAIN A909 frame: 1
LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSFTFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
VYDFLCHLENK

SEQ ID NO. 6214
STRAIN H36B frame: 3
KAFELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSFTFPYIPKYREAAATFN
EDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPKDYFDY
VMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSIFDGYHPA
KIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQKVYDFLCH
LENK

SEQ ID NO. 6215
STRAIN 18RS21 frame: 1
LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSFTFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFTYQDIINHPDSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
VYDFLCHLENK

SEQ ID NO. 6216
STRAIN M732 frame: 1
LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSFTFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFTYQDIINHPDSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
VYDFLXHLENK

SEQ ID NO. 6217
STRAIN COH1 frame: 1
LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSFTFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFTYQDIINHPDSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
VYDFLWHLENK

SEQ ID NO. 6218
STRAIN M781 frame: 1
LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSFTFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFTYQDIINHPDSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
VYDFLCHLENK

SEQ ID NO. 6219
STRAIN CJB110 frame: 1
LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSFTFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
VYDFLCHLENK

SEQUENCE LISTING

SEQ ID NO. 6220
STRAIN 1169NT frame: 2
IKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSFTFPYIPKYREAAATF
NEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPKDYFD
YVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFTYQDIINHPDSIFDGYHP
AKIKNQLSLAEHLVACVIPKHYQEDYQNLVPNDLKHRVYYLDYCNETLYEWNQKVYDFLC
HLENK

SEQ ID NO. 6221
STRAIN JM9130013 frame: 1
IGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSFTFPYIPKYREAAATFNEDGISLT
SDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPKDYFDYVMLNWSN
TNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSIFDGYHPAKIKNQLS
LAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQKVYDFLCHLENK

SEQ ID NO. 6222
STRAIN 090 frame: 3
DYPLIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSFTFPYIPKYREA
AATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPK
DYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSIFD
GYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQKVY
DFLCHLENK

SEQ ID NO. 6301
STRAIN 2603
ATGAAAAGTCGAAAAAAAGATAAATTGGTATTGAGGTTAACAACAACACTATTGGTTTTT
GGTTTGGGTGGGGTTTGGTTTTATAATTATAAAAATGATAATGTCGAACCGACAGTCACT
AGTGCATCGGATCAAACGACGACTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATT
TCTAAGACCTATGATTTGTATGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCC
AGTGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAA
TATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGGCAATATGACT
CAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTCACTATATGATTATGCT
GAGTTAGTATCTAGTCAAAAGTATGCATCTGTTTGGAAATCAAATACCTCTTCTTATAAG
GATGCTACTGCAGCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTA
AACCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6302
STRAIN 090
GGGGTTTGGTTTTATAATTATAA
AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
ATGCATCTGTTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6303
STRAIN A909
GGGGTTTGGTTTTATAATTATAA
AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
ATGCATCTGCTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQUENCE LISTING

SEQ ID NO. 6304
STRAIN H36B
GGGGTTTGGTTTTATAATTATAAAAATGATA
ATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATT
CAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTA
TGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAGTGGACAAT
CAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAA
TATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGG
CAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTG
CTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTaTGCATCT
GCTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCAGCTCTAAC
AGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTA
TTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6305
STRAIN 18RS21
GGGGTTTGGTTTTATAATTATAAAAATGATAATG
TCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA
ACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTATGC
GTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAGTGGACAATCAG
ATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATAT
AAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGGCAA
TATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTT
CACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCATCTGTT
TGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGG
TCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTATTG
AAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6306
STRAIN M732
GGGGTTTGGTTTTATAATTATAA
AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
ATGCATCTGTTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6307
STRAIN COH1
GGGGTTTGGTTTTATAATTATAA
AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
ATGCATCTGTTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6308
STRAIN M781
GGGGTTTGGTTTTATAATTATAAAAATGA
TAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTA
TTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTG
TATGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAGTGGACA
ATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAG
AATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAA

SEQUENCE LISTING

GGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTC
TGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCAT
CTGTTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCAGCTCTA
ACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAAT
TATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6309
STRAIN CJB110
GGGGTTTGGTTTTATAATTATAAAAATGATAATGT
CGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAAA
CGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTATGCG
TCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAGTGGACAATCAGA
TTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATATA
AAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGGCAAT
ATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTC
ACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCATCTGTTT
GGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGGT
CTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTATTGA
AACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6310
STRAIN 1169NT
GGGGTTTGGTTTTATAATTATAAAAATGATAATGT
CGAACAGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAAA
CGATTTCCCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTATGCG
TCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAGTGGACAATCAGA
TTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATATA
AAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGGCAAT
ATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTC
ACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCATCTGTTT
GGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGGT
CTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTATTGA
AACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6311
STRAIN JM9130013
TTTGGTTTTATAATTATAAAAATGATAATGTCGAACCGACAGTCACTAGT
GCATCGGATCAAACGACGACTTTTATTCAAACGATTTCCCCAACAGCTAT
TGAAATTTCTAAGACCTATGATTTGTATGCGTCAGTCTTATTAGCACAAG
CTATTTTGGAATCATCCAGTGGACAATCAGATTTGTCTAAGGCTCCTAAT
TATAACCTCTTTGGCATCAAAGGAGAATATAAAGGTAAATCTGTTCAAAT
GCCTACTTTAGAAGATGATGGGAAAGGTAATATGACCCAAATCCAAGCTC
CTTTTCGCGCCTATCCAAATTATTCTGCTTCACTATATGATTATGCTGAG
TTAGTATCTAGTCAAAAGTATGCATCTGTTTGGAAATCAAATACCTCTTC
TTATAAGGATGCTACTGCAGCTCTAACAGGTCTTTATGCGACAGATACTG
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TATGATAAA

SEQ ID NO. 6312
STRAIN 2603 frame: 1
MKSRKKDKLVLRLTTTLLVFGLGGVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEI
SKTYDLYASVLLAQAILESSSGQSDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMT
QIQAPFRAYPNYSASLYDYAELVSSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKL
NQIIETYSLDAYDK

SEQ ID NO. 6313
STRAIN 090 frame: 1
GVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6314
STRAIN A909 frame: 1
GVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ

SEQUENCE LISTING

SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASAWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6315
STRAIN H36B frame: 1
GVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASAWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6316
STRAIN 18RS21 frame: 1
GVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6317
STRAIN M732 frame: 1
GVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6318
STRAIN M781 frame: 1
GVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6319
STRAIN CJB110 frame: 1
GVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6320
STRAIN 1169NT frame: 1
GVWFYNYKNDNVEQTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6321
STRAIN JM9130013 frame: 3
WFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQSD
LSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELVSS
QKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIENYSLDAYDK

SEQ ID NO. 6401
STRAIN 2603
ATGAACAAGTCTAAGAAAATCGAAAATTATCAATTATTATTACTACAAGCGCAAGCTCTA
TTCTCAGATGAAACAAATGCTCTTGCCAACTTATCAAATGCTTCAGCTATGCTAAATGCT
ATGCTTCCAAATTCTGTATTTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTT
GGCCCTTTCCAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGT
GAATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATGCTAACTAT
ATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCTATGTTTAAAAATGGCAAA
CTTCTAGGAGTTCTAGATTTAGATTCTTCTTTAGTAGCAGATTATGATGAGATTGATCAA
GAATACTTAGAAAAATTTGTAGGTATTCTAGTAGAACATACGATTTGGAATTTGGATATG
TTTGGAGTTGAAAAG

SEQ ID NO. 6402
STRAIN 090
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTAC
AGGCTTTTATTTATTTGATGGAAAGGAGTTAATTCTTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGAA
TCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC

TAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCTA
TGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAATTTGGATA

SEQ ID NO. 6403
STRAIN A909
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAA
CTTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTAT
TTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCTTTC
CAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGG
TGAATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGC
ATGCTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTA
CCTATGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTC
TTTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTG
TAGGTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTT
GAAAAG

SEQ ID NO. 6404
STRAIN H36B
CTCTATTCTCAGATGAAACAAATGCTCTTGC
CAACTTATCAAATGCTTCAGCTATGCTAAaTGCTATGCTTCCAAATTCTG
TATTTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCT
TTCCAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTG
TGGTGAATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAA
AGCATGCTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTA
GTACCTATGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTC
TTCTTTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAAT
TTGTAGGTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGA
GTTGAAAAG

SEQ ID NO. 6405
STRAIN 18RS21
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTA
CAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCTTTCCAG
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
ATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATG
CTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCT
ATGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTCTTT
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG
GTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAA
AAG

SEQ ID NO. 6406
STRAIN M732
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTA
CAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGGCCCTTTTCAG
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
ATCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATG
CTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCC
ATGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTCTTT
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG
GTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAA
AAG

SEQ ID NO. 6407
STRAIN COH1
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAAC
TTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATT
TACAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGGCCCTTTTC
AGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGT
GAATCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCA

TGCTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTAC
CCATGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTCT
TTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGT
AGGTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTG
AAAAG

SEQ ID NO. 6408
STRAIN M781
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTA
CAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGGCCCTTTTCAG
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
ATCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATG
CTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCC
ATGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTCTTT
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG
GTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAA
AAG

SEQ ID NO. 6409
STRAIN CJB110
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTAC
AGGCTTTTATTTATTTGATGGAAAGGAGTTAATTCTTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGAA
TCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCTA
TGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAAA
AG

SEQ ID NO. 6410
STRAIN 1169NT
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTAC
AGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGAA
TCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCCA
TGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAAA
AG

SEQ ID NO. 6411
STRAIN JM9130013
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTAC
AGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGAA
TCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCTA
TGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAAA
AG
SEQ ID NO. 6412
STRAIN 2603 frame: 1
MNKSKKIENYQLLLLQAQALFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELIL
GPFQGGVSCVHITLGKGVCGESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGK
LLGVLDLDSSLVADYDEIDQEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6413

STRAIN 090 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGKELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLD

SEQ ID NO. 6414
STRAIN A909 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6415
STRAIN H36B frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6416
STRAIN 18RS21 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6417
STRAIN M732 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6418
STRAIN COH1 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6419
STRAIN M781 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6420
STRAIN M781 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6421
STRAIN CJB110 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGKELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6422
STRAIN 1169NT frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6423
STRAIN JM9130013 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQUENCE LISTING

SEQ ID NO. 6501
STRAIN 2603
ATGAAAAAGAGTACCCAAATAATACTACTAATAGTTGCA
TTATTCATACTTGTTTTTAGCGGAGGATTTTATATGAAAGAACAACAAAGAAAAGAAGAA
CTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATTGAAAAATTCCTATGAG
AATATAGAAGAAATAAAAATCACACATCCTGTTTCAACTGAAATTCCTGGAGATTGGCAT
TGTACTGTAAAGATTTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAAT
TTGGAATCGAAAAAAAATTATAGCGGAAAATTTAATGAAAAAAATATGAATTTTTTTGAT
TCAAGAATTGGTAAAACAAAAAAAACTATAAAAATTATTTTTTCAGATGGTCAGGAGAAG
ATACAA

SEQ ID NO. 6502
STRAIN 090
GGAGGATTTTATATGAAAGAACA
ACAAAGAAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAG
TCAAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACA
CATCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGAT
TTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGG
AATCGAAAAAAAATTATAGCGGAAATTTTAATGAAAAAAATATGAATTTT
TTTGATTCAAGAATTGGTAAAACAAAAAAAACTATAAAAATTATTTTTTC
AGAtGGtCAGGAGAAGATaCAA

SEQ ID NO. 6503
STRAIN A909
GGAGGATTTTATATGAAAGAACAACAA
AGAAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAA
AGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACACATC
CTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCA
TTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATC
GAAAAAAAATTATAGCGGAAAATTTAATGAAAAAAATATGAATTTTTTTG
ATTCAAGAATTGGTAAAACAAAAAAAACTATAAAAATTATTTTTTCAGAT
GGtCAGGAGAAGATACAA

SEQ ID NO. 6504
STRAIN H36B
GGAGGATTTTATATGAAAGAACA
ACAAAGAAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAG
TCAAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACA
CATCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGAT
TTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGG
AATCGAAAAAAAATTATAGCGGAAAATTTAATGAAAAAAATATGAATTTT
TTTGATTCAAGAATTGGTAAAACAAAAAAAACTATAAAAATTAtTTTTTC
AGATGGtCAGGAGAAGATaCAA

SEQ ID NO. 6505
STRAIN 18RS21
GGAGGATTTTATATGAAAGAACAAC
AAAGAAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTC
AAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACACA
TCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTT
CATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAA
TCGAAAAAAAATTATAGCGGAAAATTTAATGAAAAAAATATGAATTTTTT
TGATTCAAGAATTGGTAAAACAAAAAAAACTATAAAAATTATTTTTTCAG
ATGGtCAGGAGAAGATaCAA

SEQ ID NO. 6506
STRAIN M781
GGAGGATTTTATATGAAAGAACAACAAAGAAAA
GAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATT
GAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACACATCCTGTTT
CAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCATTTAAT
GATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATCGAAAAA
AAATTATAGCGGAAAATTTAATGAAAAAAATATGAATTTTTTTGATTCAA

GAATTGGTAAAACAAAAAAAACTATAAAAATTATTTTTTCAGATGGTCAG
GAGAAGATACAA

SEQ ID NO. 6507
STRAIN CJB110
GGAGGATTTTATATGAAAGAACAACAAAGAAAAGAAGAA
CTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATTGAAAAA
TTCCTATGAGAATATAGAAGAAATAAAAATCACACATCCTGTTTCAACTG
AAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCATTTAATGATAAA
AAATCTATTGTTTATAATATTACACATAATTTGGAATCGAAAAAAAATTA
TAGCGGAAATTTTAATGAAAAAAATATGAATTTTTTTGATTCAAGAATTG
GTAAAACAAAAAAAACTATAAAAATTATTTTTTCAGATGGTCAGGAGAAG
ATACAA

SEQ ID NO. 6508
STRAIN 1169NT
GGAGGATTTTATATGAAAGAACAACAAAG
AAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAG
CATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACACATCCT
GTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCATT
TAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATCGA
AAAAAAATTATAGTGGAAAATTTAATGAAAAAAATATGAATTTTTTTGAT
TCAAGAATTGGTAAAACAAAAAAAACTATAAAAATTATTTTTTCAGATGG
TCAGGAGAAGATACAA

SEQ ID NO. 6509
STRAIN JM9130013
GGAGGATTTTATATGAAAGAACAAC
AAAGAAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTC
AAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACACA
TCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTT
CATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAA
TCGAAAAAAAATTATAGCGGAAAATTTAATGAAAAAAATATGAATTTTTT
TGATTCAAGAATTGGTAAAACAAAAAAAACTATAAAAATTATTTTTTCAG
AtGGtCAGGAGAAGATACAA

SEQ ID NO. 6510
STRAIN 2603 frame: 1
MKKSTQIILLIVALFILVFSGGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKI
THPVSTEIPGDWHCTVKISFNDKKSIVYNITHNLESKKNYSGKFNEKNMNFFDSRIGKTK
KTIKIIFSDGQEKIQ

SEQ ID NO. 6511
STRAIN 090
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGD
WHCTVKISFNDKKSIVYNITHNLESKKNYSGNFNEKNMNFFDSRIGKTKKTIKIIFSDGQ
EKIQ

SEQ ID NO. 6512
STRAIN A909
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWH
CTVKISFNDKKSIVYNITHNLESKKNYSGKFNEKNMNFFDSRIGKTKKTIKIIFSDGQEK
IQ

SEQ ID NO. 6513
STRAIN H36B
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGD
WHCTVKISFNDKKSIVYNITHNLESKKNYSGKFNEKNMNFFDSRIGKTKKTIKIIFSDGQ
EKIQ

SEQ ID NO. 6514
STRAIN 18RS21
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDW
HCTVKISFNDKKSIVYNITHNLESKKNYSGKFNEKNMNFFDSRIGKTKKTIKIIFSDGQE

KIQ

SEQ ID NO. 6515
STRAIN CJB110
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVK
ISFNDKKSIVYNITHNLESKKNYSGNFNEKNMNFFDSRIGKTKKTIKIIFSDGQEKIQ

SEQ ID NO. 6516
STRAIN JM9130013
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDW
HCTVKISFNDKKSIVYNITHNLESKKNYSGKFNEKNMNFFDSRIGKTKKTIKIIFSDGQE
KIQ

SEQ ID NO. 6517
STRAIN 1169NT frame: 1
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF
NDKKSIVYNITHNLESKKNYSGKFNEKNMNFFDSRIGKTKKTIKIIFSDGQEKIQ

SEQ ID NO. 6518
STRAIN M781 frame: 1
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF
NDKKSIVYNITHNLESKKNYSGKFNEKNMNFFDSRIGKTKKTIKIIFSDGQEKIQ

SEQ ID NO. 6601
STRAIN 2603
TTGACAAGGCATATAAAAATTTCTATACTAAATTTACAAAATGAAGGAGAGGGAACTATG
GAAATACTGATTGCAGGTGGTAGTGGTTTTTTAGGAAAGCAGATAATAAAAGCAGCGCTT
ACAAAAGGGCATAAAGTGGCTTACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAG
GATCCTAGATTAACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAA
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAATCAACTAGAT
GAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGTCACAAAAATCAAATACCA
AAGTTAGTTTATATTTCAGCCAACAGCGGCTATTCAGCTTACATTAAAAGTAAAAGGAAG
GCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATG
TATGGTGAAGAGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCAT
TTGCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGTGATAGTGGCA
GAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAAATCCTTTCTATTGAAGAA
TTAAATAATAAA

SEQ ID NO. 6602
STRAIN 090
ACAAGGCATATAAAAATTTCTATACTAAATTTACAAAAT
GAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTT
AGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT
ACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTA
ACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAAGA
CAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAATC
AACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGT
CACAAAAATCAAATACCAAAGTTAGTTTATATTTCAGCCAACAGCGGCTA
TTCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAA
GCGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTGAAGAG
CGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCATTT
GCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGTGA
TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA
ATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO: 6603
STRAIN A909
ACAAGGCATATAAAAATTTCTATACTAAATTTACAAAATG
AAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTTA
GGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTTA
CTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTAA
CCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAAGAC
AGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAATCA
ACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGTC

SEQUENCE LISTING

ACAAAAATCAAATACCAAAGTTAGTTTATATTTCAGCCAACAGCGGCTAT
TCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAAG
CGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTGAAGAGC
GACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCATTTG
CCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGTGAT
AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAAA
TCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6604
STRAIN H36B
TATAAAAATTTCTATACTAAATTTACAAAATGAAGGAGAGGGAACTATGG
AAATACTGATTGCAGGTGGTAGTGGTTTTTTAGGAAAGCAGATAATAAAA
GCAGCGCTTACAAAAGGGCATAAAGTGGCTTACTTATCAAGACATGAAGG
TAAAGGTGATATATTTAAGGATCCTAGATTAACCTACATTAGGGGAGATA
TTACAGAAGCTGATAAGATTCATTTAGAAGACAGAACTTTTGATATATTA
ATTGACTGTATTGGAGCGATTAAGCCCAATCAACTAGATGAGCTTAACGT
TAAAGCAACCCAAAAAGCAGTAGCACTCTGTCACAAAAATCAAATACCAA
AGTTAGTTTATATTTCAGCCAACAGCGGCTATTCAGCTTACATTAAAAGT
AAAAGGAAGGCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTTT
TGTAAGACCAGGTTTGATGTATGGTGAAGAGCGACCTCTCTCGATTTTCC
AAGCCAAGTGTATAAAGTTATTTAGTCATTTGCCTTTCTTAGGTATTGTT
GTACAAAAGGTCTTTCCAACTAAGGTTGTGATAGTGGCAGAAGCAATCGT
TACTACGCTTAGGAAAAAACCAACCCAAAAAATCCTTTCTATTGAAGAAT
TAAATAATAAA

SEQ ID NO. 6605
STRAIN 18RS21
ACAAGGCATATAAAAATTTCTATACTAAATTTACAAAAT
GAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTT
AGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT
ACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTA
ACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAAGA
CAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAATC
AACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGT
CACAAAAATCAAATACCAAAGTTAGTTTATATTTCAGCCAACAGCGGCTA
TTCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAA
GCGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTGAAGAG
CGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCATTT
GCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGTGA
TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA
ATCCTTTCTATTGAAGAATTAAATaATAAA

SEQ ID NO. 6606
STRAIN M732
CAAAATGAAGGAGAgGGAACTATGgAAATACTGATTGCAGGTGGTAGTGG
TTTTCTAGGGAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGG
TGGCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCcT
AGATTAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCATTT
AGaACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAGC
CCAATCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCA
CTCTGTCACAAAAATCAAATACCAAAGTTAGTTTACATTTCAGCCAATAG
CGGCTATTCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCA
AAGCAAGCGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGT
GAAGAGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAATTATTTAG
TCATTTGCCTTTCTTAGGTATTGTTGTACAAAAAGTCTTTCCAACTAAGG
TTGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAAACCAACT
CAAAAAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6607
STRAIN COH1
ACAAGGCATATAAAAATTTCTATACTAAATTTAC
AAAATGAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGT
TTTCTAGGGAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGGT
GGCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCTA

GATTAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCATTTA
GAACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCC
CAATCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCAC
TCTGTCACAAAAATCAAATACCAAAGTTAGTTTACATTTCAGCCAATAGC
GGCTATTCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAA
AGCAAGCGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTG
AAGAGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAATTATTTAGT
CATTTGCCTTTCTTAGGTATTGTTGTACAAAAAGTCTTTCCAACTAAGGT
TGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAAACCAACTC
AAAAAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6608
STRAIN M781
ACAAGGCATATAAAAATTTcTATACTAAATTTaCA
AAATGAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTT
TTCTAGGGAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGGTG
GCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCTAG
ATTAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCATTTAG
AACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCC
AATCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACT
CTGTCACAAAAATCAAATACCAAAGTTAGTTTACATTTCAGCCAATAGCG
GCTATTCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAA
GCAAGCGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTGA
AGAGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAATTATTTAGTC
ATTTGCCTTTCTTAGGTATTGTTGTACAAAAAGTCTTTCCAACTAAGGTT
GTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAAACCAACTCA
AAAAATCCTTTCTAtTGAAGAATTAAATAATAAA

SEQ ID NO. 6609
STRAIN 1169NT
ACAAGGCATATAAAAATTTCTATACTAAATTTACAAA
ATGAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTT
TTAGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGTTGGC
TTACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGAT
TAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAA
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAA
TCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCT
GTCACAAAAATCAAATACCAAAGTTAGTTTACATTTCAGCCAACAGCGGC
TATTCAGCTTACATTAGAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGC
AAGCGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTGAAG
AGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAATTATTTAGTCAT
TTGCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGT
GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGACAAAACCAACTCAAA
AAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6610
STRAIN CJB110
ACAAGGCATATAAAAATTTCTATACTAAATTTACAAA
ATGAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTT
TTAGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGTGGC
TTACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGAT
TAACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAA
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAA
TCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCT
GTCACAAAAATCAAATACCAAAGTTAGTTTATATTTCAGCCAACAGCGGC
TATTCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGC
AAGCGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTGAAG
AGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCAT
TTGCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGT
GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAA
AAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6611
STRAIN JM9130013

SEQUENCE LISTING

ACAAGGCATATAAAAATTTCTATACTAAATTTACAAAATG
AAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTA
GGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTTA
CTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTAA
CcTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAAGAC
AGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAATCA
ACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGTC
ACAAAAATCAAATACCAAAGTTAGTTTATATTTCAGCCAACAGCGGCTAT
TCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAAG
CGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTGAAGAGC
GACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCATTTG
CCtTTCTTAgGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGTGAT
AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAAA
TCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6612
STRAIN 2603 frame: 1
TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6613
STRAIN 090 frame: 1
TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6614
STRAIN A909 frame: 1
TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6615
STRAIN H36B frame: 2
IKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKDPRL
TYIRGDITEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPKLVY
ISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHLPFL
GIVVQKVFPTKVVIVAEAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6616
STRAIN 18RS21 frame: 1
TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6617
STRAIN M732 frame: 1
QNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKDPRLTYIKGDIT
EADKIHLEHRNFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPKLVYISANSGYS
AYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHLPFLGIVVQKVF
PTKVVIVAEAIVTSLRKKPTQKILSIEELNNK

SEQ ID NO. 6618
STRAIN COH1 frame: 1
TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIKGDITEADKIHLEHRNFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTSLRKKPTQKILSIEELNNK

SEQUENCE LISTING

SEQ ID NO. 6619
STRAIN M781 frame: 1
TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIKGDITEADKIHLEHRNFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTSLRKKPTQKILSIEELNNK

SEQ ID NO. 6620
STRAIN 1169NT frame: 1
TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKLAYLSRHEGKGDIFKD
PRLTYIKGDITEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIRSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTTLRTKPTQKILSIEELNNK

SEQ ID NO. 6621
STRAIN CJB110 frame: 1
TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6622
STRAIN JM9130013 frame: 1
TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6701
STRAIN 090
CAATAACAACATTTGAAAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGA
TCTGGAGAAGCCGCTGCACGTTTGTTAGCTAAGTTAGGAGCAATAGTGAC
AGTTAATGATGGCAAACCATTTGATGAAAATCCAACAGCACAGTCTTTGT
TGGAAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTA
GATGAGGATTTTTGTTACATGATTAAAAATCCAGGAATACCTTATAACAA
TCCTATGGTCAAAAAAGCATTAGAAAAACAAATCCCTGTTTTGACTGAAG
TGGAATTAGCATACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGC
TCTAACGGGAAAACGACAACGACAACGATGATTGCAGAAGTCTTAAATGC
TGGAGGTCAGAGAGGTTTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTG
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TACTAATTTAATGCCAACTCATTTAGATTATCATGGGTCTTTTGAAGATT
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TTGGTACTTAATTTTAATCAAGGTATTTCTAAAGAGTTAGcTAAAACTAC
TAAAGCAACAATCGTTCCTTTCTCTACTACGGAAAAAGTTGATGGTGCTT
ACGTACAAGACAAGCAACTTTTCTATAAAGGGGAGAATATTATGTTAGTA
GATGACATTGGTGTCCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAAC
TATTGCGGTTGCTAAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAA
CTTTAAGCAATTTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAG
GTTCATGGTATTAGTTTCTATAACGACAGCAAGTCAACTAATATATTGGC
AACTCAAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTG
CAGGAGGTCTTGATCGCGGTAATGAGTTTGATGAATTGATACCAGATATC
ACTGGACTTAAACATATGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAA
ACGTGCTGCACAAAAAGCAGGAGTAACTTATAGCGATGCTTTAGATGTTA
GAGATGCGGTACATAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATC
TTGCTAAGTCCTGCAAATGCATCATGGGACATGTATAAGAATTTCGAAGT
CCGTGGTGATGAATTCATTGATACtTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6702
STRAIN A909
CAATAACAACATTTGAAAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGA
TCTGGAGAAGCTGCTGCACGTTTGTTAGCTAAGTTAGGAGCAATAGTGAC
AGTTAATGATGGCAAACCATTTGATGAAAATCCAACAGCACAGTCTTTGT
TGGAAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTA

SEQUENCE LISTING

GATGAGGATTTTTGTTACATGATTAAAAATCCAGGAATACCTTATAACAA
TCCTATGGTCAAAAAAGCATTAGAAAAACAAATCCCTGTTTTGACTGAAG
TGGAATTAGCATACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGC
TCTAACGGGAAAACGACAACGACAACGATGATTGCAGAAGTCTTAAATGC
TGGAGGTCAGAGAGGTTTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTG
AAGTTGTTCAGGCTGCGAATGATAAAGATACTCTAGTTATGGAATTATCA
AGTTTTCAGCTAATGGGAGTTAAGGAATTTCGTCCTCATATTGCAGTAAT
TACTAATTTAATGCCAACTCATTTAGATTATCATGGGTCTTTTGAAGATT
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TTGGTACTTAATTTTAATCAAGGTATTTCTAAAGAGTTAGCTAAAACTAC
TAAAGCaACAATCGTTCCTTTCTCTACTACGGAAAAAGTTGATGGTGCTT
ACGTACAAGACAAGCAACTTTTCTATAAAGGGGAGAATATTATGTCAGTA
GATGACATTGGTGTCCCAGGAAGCCATAACGTAnAGAATGCTCTAGCAAC
TATTGCGGTTGCTAAACTGGCTGGTATCAGTAATCAAGTTATTAgAGAAA
CTTTAAGCAATTTTGGAGGtGTTAAACACCGCTTGCAATCACTCGGTAAG
GTTCATGGTATTAGTTTCTATAACGACAGCAAGTCAACTAATATATTGGC
AACTCAAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTG
CAGGAGGTCTTGATCGCGGTAATGAGTTTGATGAATTGATACCAGATATC
ACTGGACTTAAACATATGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAA
ACGTGCTGCACAAAAAGCAGGAGTAACTTATAGCGATGCTTTAGATGTTA
GAGATGCGGTACATAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATC
TTGCTAAGTCCTGCAAATGCATCATGGGACATGTATAAGAATTTCGAAGT
CCGTGGTGATGAATTCATTGATACTTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6703
STRAIN H36B
GGACGAGTAATGAAAACAATAACAACATTTGAAAAT
AAAAAAGTTTTAGTCCTTGGTTTAGCACGATCTGGAGAAGCTGCTGCACG
TTTGTTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACCAT
TTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAAAGTG
GTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTTGTTACAT
GATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAAGCAT
TAGAAAAACAAATCCCTGTTTTGACTGAAGTGGAATTAGCATACTTAGTT
TCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAACGACAAC
GACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTCAGAGAGGTTTGT
TAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTCAGGCTGCGAAT
GATAAAGATACTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGGGAGT
TAAGGAATTTCGTCCTCATATTGCAGTAATTACTAATTTAATGCCAACTC
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ATCCAAAATCAAATGTCTTCATCTGATTTTTTGGTACTTAATTTTAATCA
AGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAATCGTTCCTT
TCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGCAACTT
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SEQ ID NO. 6704
STRAIN 18RS21
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SEQUENCE LISTING

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SEQ ID NO. 6705
STRAIN M732
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SEQ ID NO. 6706
STRAIN COH1
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SEQ ID NO. 6707
STRAIN M781
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SEQ ID NO. 6708
STRAIN CJB110
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SEQUENCE LISTING

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SEQ ID NO. 6709
STRAIN 1169NT
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SEQ ID NO. 6710
STRAIN JM9130013
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SEQ ID NO. 6710
STRAIN 2603
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SEQ ID NO. 6711
STRAIN 090 frame: 3
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SEQ ID NO. 6712
STRAIN A909 frame: 3
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SEQ ID NO. 6713
STRAIN H36B frame: 1
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SEQ ID NO. 6714
STRAIN 18RS21 frame: 1
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SEQ ID NO. 6715
STRAIN M732 frame: 1
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SEQ ID NO. 6716
STRAIN COH1 frame: 1
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SEQ ID NO. 6717
STRAIN M781 frame: 1
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SEQ ID NO. 6718
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SEQ ID NO. 6719
STRAIN 1169NT frame: 3
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SEQUENCE LISTING

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STTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISNQVIRET
LSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLDRGNEFD
ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSNALDVRDAVHKAYEVAQQGDVILXSP
ANASWDMYKNFEVRGDEFIDTF

SEQ ID NO. 6720
STRAIN JM9130013 frame: 1
GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGI
TGSNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNQMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
RSNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6721
STRAIN 2603 frame: 1
GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGI
TGSNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNQMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6801
STRAIN 2603
ATGGCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGGGACTTTTTGATACACGAGAG
CAAGCGAAACGTGGTGTTATGGCAGGAATGGTGATTAACGTTATCAATGGAGAACGTTAT
GATAAACCAGGTGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTA
AAATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTGAAATTTCA
GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTTACTGATGTTATG
CTACAATCAGGAGCGCGTTTAGTTTACGCAGTAGATGTAGGAACAAATCAATTAGTTTGG
AAGTTACGTCAGGATCATCGTGTTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAA
AAAGAAGATTTCAAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCT
CTTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAGTAGTGGCA
TTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGTAAAAATGGTATTGTCAAA
GACAAGTTGGTTCATGAAAAGGTTTTGACAACAGTGACCAATTTCACGAAAGATTATGGA
TATACGGTTAAACATCTTGATTTTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTT
TTAATGCATTTGCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGAT
GTTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6802
STRAIN 090
GCTAAAGAGAGGGTAGATGTTCTTGCCT
ATAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATG
GCAGGAATGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGG
TGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAA
AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTT
GAAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG
TAGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGT
GTTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTT
CAAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTC
TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA
GTAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGG
TAAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAA
CAGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGAT
TTTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTT

SEQUENCE LISTING

GCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATG
TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6803
STRAIN A909
GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATGG
CAGGAATGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGT
GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTTC
AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
TAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6804
STRAIN H36B
GCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGG
GACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATGGCAGGAATG
GTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGTGAAAAGGT
TGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAAAATATGTTA
GTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTGAAATTTCA
GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTTAC
TGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGTAGATGTAG
GAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGTGTTCGTTCT
ATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTTCAAGGAGGG
ACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCTTAATTTGA
TTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAGTAGTGGCA
TTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGTAAAAATGG
TATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAACAGTGACCA
ATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATTTTTCGCCC
ATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTGCAAAAGTG
TCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGTTATAGAAA
AAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6805
STRAIN 18RS21
GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATGG
CAGGAATGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGT
GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTTC
AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
TAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6806

SEQUENCE LISTING

STRAIN M732
GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATGG
CAGGACTGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGC
GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTTC
AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
TAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCGTTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6807
STRAIN COH1
GCTAAAGAGAGGGTAGATGTTCTTGCCT
ATAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATG
GCAGGACTGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGG
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AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTT
GAAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG
TAGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGT
GTTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTT
CAAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTC
TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA
GTAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGG
TAAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAA
CAGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGAT
TTTTCGCCCGTTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTT
GCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATG
TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6808
STRAIN M781
GCTAAAGAGAGGGTAGATGTTCTTGCCT
ATAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATG
GCAGGACTGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGG
CGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAA
AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTT
GAAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG
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CAAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTC
TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA
GTAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGG
TAAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAA
CAGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGAT
TTTTCGCCCGTTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTT
GCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATG
TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6809
STRAIN CJB110
GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATGG
CAGGAATGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGT

SEQUENCE LISTING

GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTTC
AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
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AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6810
STRAIN 1169NT
GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATGG
CAGGACTGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGC
GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGTG
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AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
TAATTTGATTTTGCCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
TAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6811
STRAIN JM9130013
GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATGG
CAGGAATGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGT
GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
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AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
TAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6812
STRAIN 2603 frame: 1
MAKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6813

SEQUENCE LISTING

STRAIN 090 frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6814
STRAIN A909 frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6815
STRAIN 18RS21 frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6816
STRAIN M732 frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6817
STRAIN COH1 frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6818
STRAIN M781 frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6819
STRAIN CJB110 frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6820
STRAIN 1169NT frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6821

SEQUENCE LISTING

STRAIN JM9130013 frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6822
STRAIN H36B frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6901
STRAIN 2603
ATGAATAAAAAGGTACTATTGACATCGACAATGGCAGCTTCGCTATTATCAGTCGCAAGT
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GATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATACACTAAGC
GTTATTTCAGAAGCAATGTCAATTGATATGAATGTCTTAGCAAAAATAAATAACATTGCA
GATATCAATCTTATTTATCCTGAGACAACACTGACAGTAACTTACGATCAGAAGAGTCAT
ACTGCCACTTCAATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCT
ACTGTGGATTTGAAAACCAATCAAGTTTCTGTTGCAGACCAAAAAGTTTCTCTCAATACA
ATTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCAATGAAGACATAT
TCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGCACAAGAGCAAGCTGTTAGTCAA
GCAGCAGCTAATGAACAGGTATCACCAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCA
GCAGCTAAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCA
CCAGCTTCTGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAACT
GTAGCAGCCCCTAGAGTGGCAAGTGTTAAAGTAGTCACTCCTAAAGTAGAAACTGGTGCA
TCACCAGAGCATGTATCAGCTCCAGCAGTTCCTGTGACTACGACTTCACCAGCTACAGAC
AGTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCCGGTAGCACAAAAAGCTCCAACAGCA
ACACCGGTAGCACAACCAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCA
GGGCTCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAAT
GAATTCAGTACATACCGTGCGGGAGATCCAGGTGATCATGGTAAAGGTTTAGCAGTTGAC
TTTATTGTAGGTACTAATCAAGCACTTGGTAATAAAGTTGCACAGTACTCTACACAAAAT
ATGGCAGCAAATAACATTTCATATGTTATCTGGCAACAAAAGTTTTACTCAAATACAAAC
AGTATTTATGGACCTGCTAATACTTGGAATGCAATGCCAGATCGTGGTGGCGTTACTGCC
AACCACTATGACCACGTTCACGTATCATTTAACAAATAATATAAAAAAGGAAGCTATTTG
GCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAATTTTTATTA

SEQ ID NO. 6902
STRAIN 090
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SEQ ID NO. 6903
STRAIN A909
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SEQ ID NO. 6904
STRAIN H36B
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TAATTTTTATTA

SEQ ID NO. 6905
STRAIN 18RS21
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AAATCATCATATACTGTGAAATATGGTGATACAcTAAGcGTTATTTCAGA
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TCGTGGTGGCGTTACTGCCAACCACTATGACCACGTTCACGTATCATTTA
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SEQ ID NO. 6906
STRAIN COH1
CTGATTT
GGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATACAC
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CACCAGCAACAAATGCTGCTGGTCAAACAACAGcTACTGTCGATTTGAAA
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CaTATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGCACAAGAG
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A

SEQ ID NO. 6907
STRAIN M732
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CACTGACAGTAACTTACGATCAGAAGAGTCAtACTGCCACTTCAATGAAA
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SEQUENCE LISTING

CAATTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCA
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SEQ ID NO. 6908
STRAIN M781
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TTTTATTA

SEQ ID NO. 6909
STRAIN CJB110
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SEQUENCE LISTING

TAAgAACTGTAGCAGCCCCTAGAGTGGCAAGTGTTAAAGTAGTCACTCCT
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SEQ ID NO. 6910
STRAIN 1169NT
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TACTTGGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTATG
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SEQ ID NO. 6911
STRAIN JM9130013
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SEQUENCE LISTING

TGCAGGGCTCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAA
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SEQ ID NO. 6912
STRAIN 2603 frame: 1
MNKKVLLTSTMAASLLSVASVQAQETDTTWTARTVSEVKADLVKQDNKSSYTVKYGDTLS
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FIVGTNQALGNKVAQYSTQNMAANNISYVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTA
NHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6913
STRAIN 090 frame: 2
ETTLTVTYDQKSHTATSMKIETPATNAAGQTPATVDLKTNQVSVADQKVSLNTISEGMTP
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YVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYAL
NRLSRFLYNFY

SEQ ID NO. 6914
STRAIN A909 frame: 3
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
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SSAPALKSKEVLAQGQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
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SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALHRLSRFLYNFY

SEQ ID NO. 6915
STRAIN H36B frame: 3
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
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SSAPALKSKEVLAQGQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
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SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAAHPENARLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALHRLSRFLYNFY

SEQ ID NO. 6916
STRAIN 18RS21 frame: 3
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
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SSAPALKSKEVLAQEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVTPKVETGASPEHVSAPAVPVTTTSPATD
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EFSTYRAGDPGDHGKGLAVDFIVGTNQALGNKVAQYSTQNMAANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6917
STRAIN M732 frame: 3
DLVKQDNKSSYTVKYGDTXSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH

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PASVAAETPAPVAKVAPVRTVAAPRVASAKVVTPKVETGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPVAQKAPTASPVAQPASTTNAVAAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6918
STRAIN COH1 frame: 3
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
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SEQ ID NO. 6919
STRAIN M781 frame: 3
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SEQ ID NO. 6920
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SEQ ID NO. 6921
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SEQ ID. NO. 7001
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SEQ ID. NO. 7002

STRAIN H36B
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STRAIN H36B frame: 1

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SEQUENCE LISTING

QVNDTSIPAEMRENLGQYSFGYQGSTVYYRDNKGIRVGTKTEEISYYVDEE

SEQ ID. NO. 7005
STRAIN 18RS21 frame: 1
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SEQ ID. NO. 7006
STRAIN 2603 frame: 1
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SEQ ID NO. 7101
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SEQUENCE LISTING

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SEQ ID NO. 7102
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SEQ ID NO. 7103
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STRAIN H36B
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SEQ ID NO. 7105
STRAIN 18RS21
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SEQ ID NO. 7106
STRAIN M732
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SEQUENCE LISTING

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CCAAACAAAATCAAAATCTACAAAAATCAACCCTGTAACTACAATTCACA
AAAAACAATTACACCAATTTACAGCTATTAACCCTATGAGAAATTATGGC
AAACCATCAAACTCCACTACTGTAAAATCAAA

SEQ ID NO. 7108
STRAIN M781
CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACTTGA
CAATACTGGAACAGCAAATATGCCTGACGGAAAAGTTACTAATGCTGGCA
CTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAA
CAAACTAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATGGT
TGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTA
AAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAA
TTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCC
TGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGAAG
CTGCAAAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAGTTAACAAA
CAAATCCCTTACAATTGGAAACCTTACACTATTAAAAATATTCCTGTAAA
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CAAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTTAGATGAA
GCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCAA
GGCTATTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATGATATTG
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GAAACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAAACAGG
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AAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTACG
CGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGA
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TGACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAACCAGATGGA
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TCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACC
AAACAAAATCAAAATCTACAAAAATCAACCCTGTAACTACAATTCACAAA
AAACAATTACACCAATTTACAGCTATTAACCCTATGAGAAATTATGGCAA
ACCATCAAACTCCACTACTGTAAAATCAAA

SEQ ID NO. 7109
STRAIN CJB110
GACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGC
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CTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGAT
TTCAAACAAACTAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGA
TATGGTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAA
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CATGAATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAA
GGCCCCTGCTCCAGATTcTAATATAAATAATATTACGAAATCATACCCAC
ACGAAGCTGCAAAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAGTT
AACAAACAAATCCCTTACAATTGGAAACCTTACGCTATTAAAAATATTCC
TGTAAATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAG
ACATCCCAAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTTA
GATGAAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAA
TGTCAAGGCTATTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATG
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TACAAATGGTCTTGTTGGTAAAACTCGCATTGTACAAGCGCTCTCTCAAG
GAAAAGCCTATGCTGACGTACGTGGTGTCCTAGATACTGATACACAAGAT
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CACAGAGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATT
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GATGGAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAA
TATCTTACAAGTCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCA
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AATACAAATTAGTTATCAATGACTTTTTATTCGGTGGTGGTGATGGCTTT
GCAAGCTTCAGAAATGCCAAACTTCTAGGAGCCATTAATCCCGATACAGA
GGTATTTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGA
GCGTTCCAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAAT
GAAACTATTACACAAAATGATGGTACACATAGCATTATTAAGAAACTTTA
TTTAGATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTT
TAAACCAAACAAAATCAAAATCTACAAAAATCAACCCTGTAACTACAATT
CACAAAAAACAATTACACCAATTTACAGCTATTAACCCTATGAGAAATTA
TGGCAAACCATCAAACTCCACTACTGTAAAATCA

SEQ ID NO. 7110
STRAIN 1169NT
CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACTTGA
CAATACTGGAACAGCAAATATGCCTGATGGAAAAGTTGCTAATGCTGGTA
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CAAACTAACCCTAATGGTGAAAGCATTAGGGTTCAAGCAGGCGATATGGT
TGGAGCAAGTCCAGCCAACTCTGGGCTTCTTCAAGATGAACCAACTGTCA
AAAATTTTAATGCAATGAATGTTGAGTATGGCACATTGGGTAACCATGAA
TTTGATGAAGGGTTGGCAGAATATAATCGTATCGTTACTGGTAAAGCCCC
TGCTCCAGATTCTAATATTAATAATATTACGAAATCATACCCACATGAAG
CTGCAAAACAAGAAATTGTAGTGGCAAATGTTATTGATAAAGTTAACAAA
CAAATTCCTTACAATTGGAAGCCTTACGCTATTAAAAATATTCCTGTAAA
TAACAAAAGTGTGAACGTTGGCTTTATCGGGATTGTCACCAAAGACATCC
CAAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTTAGATGAA
GCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCAA
AGCTATTGTAGtTCTCGCACATGTACCTGCAACAAGTAAAAATGATATTG
CTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCCCT
GAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAA
TGGTCTTGTTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAG
CCTATGCTGATGTACGTGGTGTCTTAGATACTGATACACAAGATTTCATT
GAGACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAAACAGG
TAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAAC
AAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGTCATGATTACG
CGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGA
GGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCA
TGACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAACCAGATGGA
ACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTT
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ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGT
AAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATACA
AATTAGTTATCAATGACTTTTTATTCGGTGGTGGTGATGGCTTTGCAAGC
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TATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTTC
CAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAACT
ATTACACAAAATGATGGTACACATAGCATTATTAAGAAACTTTATTTAGA
TCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACC
AAACAAAATCAAAATCTACAAAAATCAACCCTGTAACTACAATTCACAAA
AAACAATTACACCAATTTACAGCTATTAACCCTATGAGAAATTATGGCAA
ACCATCAAACTCCACTACTGTAAAATCAAA

SEQUENCE LISTING

SEQ ID NO. 7111
STRAIN JM9130013
CGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACTTGACAATA
CTGGAACAGCAAATATGCCTGACGGAAAAGTTACTAATGCTGGCACTGCT
GCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAACAAAC
TAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATGGTTGGAG
CAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTAAAACA
TTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAATTTGA
TGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCCTGCTC
CAGATTcTAATATAAATAATATTACGAAATCATACCCACACGAAGCTGCA
AAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAGTTAACAAACAAAT
CCCTTACAATTGGAAACCTTACACTATTAAAAATATTCCTGTAAATAACA
AAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACATCCCAAAC
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AACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCAAGGCTA
TTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATGATATTGCTGAA
GGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCCCTGAAAA
TAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAATGGTC
TTGTTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAGCCTAT
GCTGATGTACGTGGTGTCCTAGATACTGATACACAAGATTTCATTGAAAC
CCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAAACAGGTAGTG
CCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAACAAGTA
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TGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGAGGCTC
AACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCATGACA
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CACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTTACAAG
TCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGAACAATAC
GACCAAAAACAAAATTTCTTCCTTCAAATAGCTGGTCTGCGATACACTTA
CACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGTAAAAG
CTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATACAAATTA
GTTATCAATGACTTTTTATTCGGTGGTGGTGATGGCTTTGCAAGCTTCAG
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CCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTTCCAAAT
AATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAACTATTAC
ACAAAATGATGGTACATATAGCATTATTGAGAAACTTTATTTAGATCGAC
AAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACCAAACA
AAATCAAAATCTACAAAAATCAACCCTGTAACTACAATTCACAAAAAACA
ATTACACCAATTTACAGCTATTAACCCTATGAGAAATTATGGCAAACCAT
CAAACTCCACTACTGTAAAATCAAAA

SEQ ID NO. 7112
STRAIN 2603 frame: 1
MKKKIILKSSVLGLVAGTSIMFSSVFADQVGVQVIGVNDFHGALDNTGTANMPDGKVANA
GTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVGASPANSGLLQDEPTVKNFNAMNVE
YGTLGNHEFDEGLAEYNRIVTGKAPAPDSNINNITKSYPHEAAKQEIVVANVIDKVNKQI
PYNWKPYAIKNIPVNNKSVNVGFIGIVTKDIPNLVLRKNYEQYEFLDEAETIVKYAKELQ
AKNVKAIVVLAHVPATSKNDIAEGEAAEMMKKVNQLFPENSVDIVFAGHNHQYTNGLVGK
TRIVQALSQGKAYADVRGVLDTDTQDFIETPSAKVIAVAPGKKTGSADIQAIVDQANTIV
KQVTEAKIGTAEVSVMITRSVDQDNVSPVGSLITEAQLAIARKSWPDIDFAMTNNGGIRA
DLLIKPDGTITWGAAQAVQPFGNILQVVEITGRDLYKALNEQYDQKQNFFLQIAGLRYTY
TDNKEGGEETPFKVVKAYKSNGEEINPDAKYKLVINDFLFGGGDGFASFRNAKLLGAINP
DTEVFMAYITDLEKAGKKVSVPNNKPKIYVTMKMVNETITQNDGTHSIIKKLYLDRQGNI
VAQEIVSDTLNQTKSKSTKINPVTTIHKKQLHQFTAINPMRNYGKPSNSTTVKSKQLPKT
NSEYGQSFLMSVFGVGLIGIALNTKKKHMK

SEQ ID NO. 7113
STRAIN 090 frame: 3
VGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRV
QAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAPDS
NINNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYAIKNIPVNNKSVNVGFIGIVTK
DIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAAEM
MKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFIE

TPSAKVVAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPV
GSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVVE
ITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPDA
KYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSVPNNKPKIY
VTMKMVNETITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHKK
QLHQFTAINPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7114
STRAIN A909 frame: 3
VNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVG
ASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAPDSNINNITK
SYPHEAAKQEIVVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIVTKDIPNLVL
RKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAAEMMKKVNQL
FPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFIETPSAKVI
AVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPVGSLITEA
QLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVVEITGRDLY
KALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPDAKYKLVIN
DFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSVPNNKPKIYVTMKMVN
ETITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHKKQLHQFTA
INPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7115
STRAIN H36B frame: 2
QVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAPD
SNINNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIVT
KDIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAAE
MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFI
ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
VGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSVPNNKPKI
YVTMKMVNETITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7116
STRAIN 18RS21 frame: 1
DQVGVQVIGVNDFHGALDNTGTANMPDGKVXNAGTAAQLDAYMDDAQKDFKQTNPNGESI
RVQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAP
DSNINNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIV
TKDIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAA
EMMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDF
IETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVS
PVGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQV
VEITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINP
DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSVPNNKPK
IYVTMKMVNETITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIH
KKQLHQFTAINPMRNYGKPSNSTTVKSK

SEQ ID NO. 7117
STRAIN M732 frame: 3
QVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAPD
SNINNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIVT
KDIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAAE
MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFI
ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
VGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSIPNNKPKI
YVTMKMVNETITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
KQLHQFTAINPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7118

SEQUENCE LISTING

STRAIN COH1 frame: 3
QVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAPD
SNINNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIVT
KDIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAAE
MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFI
ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
VGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSIPNNKPKI
YVTMKMVNETITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7119
STRAIN M781 frame: 1
QVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAPD
SNINNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIVT
KDIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAAE
MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFI
ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
VGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSIPNNKPKI
YVTMKMVNETITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7120
STRAIN CJB110 frame: 1
DQVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESI
RVQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAP
DSNINNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYAIKNIPVNNKSVNVGFIGIV
TKDIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAA
EMMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDF
IETPSAKVVAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVS
PVGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQV
VEITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINP
DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSVPNNKPK
IYVTMKMVNETITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIH
KKQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7121
STRAIN 1169NT frame: 1
QVGVQVIGVNDFHGALDNTGTANMPDGKVANAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKNFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAPD
SNINNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYAIKNIPVNNKSVNVGFIGIVT
KDIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKNDIAEGEAAE
MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFI
ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSVMITRSVDQDNVSP
VGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSVPNNKPKI
YVTMKMVNETITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7122
STRAIN JM9130013 frame: 2
GVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQ
AGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAPDSN
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SEQUENCE LISTING

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CCTTTCCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTTGGACT
TGAGCAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
ATGTTAATGAAGTTCGTGCTATTTGTGAAGAAACTGGCAATGGACATGTT
AAGTTGTTTGCTAAAATTGaAAATCAaCAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACT
AAAGTTAATGCAGCTGGTAAAGCAGTTAttACAGCAACAAATATGCTTGA
AACAATGACTGATAAACCACGTGCGACTCGTTCAGAAGTATCTGATGTCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
CATTCCCACGTAATAaCAAAACTGATGTTATTGCATCTGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACTTGTTGTGACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTCATTGATGATTAACTGGGGT
GTTATCCCTGTCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTGTAgcACTTGAAGCAGGACTTGTTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCCTGTAGGTACAGGTGGAACTAACACA
ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7212
STRAIN 2603 frame: 1
MNKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHG
DHAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQ
GIKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLI
GKQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGX
GHVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGK
AVITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATID
KNAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFR
PDADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVI

SEQUENCE LISTING

VAGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7213
STRAIN 090 frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGSDFHSYTTGTELRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7214
STRAIN A909 frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7215
STRAIN H36B frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7216
STRAIN 18RS21 frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7217
STRAIN M732 frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7218
STRAIN COH1 frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7219
STRAIN M781 frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7220
STRAIN CJB110 frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7221
STRAIN 1169NT frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7222
STRAIN JM9130013 frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGSDFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7301
STRAIN 2603
TTGTCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTATTTAGCATTAATCGGTGAT
ATCATTAATTCAAAACAGATACTTGAACGTGAAACTTTCCAACAGTCTTTTCAGCAACTA
ATGACCGAACTATCTGATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCT
GGTGATGAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGACCAT

ATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGTACAGGAAACATTATA
ACATCCATCAATTCAAATGAAAGTATCGGTGCTGATGGTCCTGCCTACTGGCATGCTCGC
TCAGCTATTAATCATATACATGATAAAAATGATTATGGAACAGTTCAAGTAGCTATTTGC
CTTGATGATGAAGACCAAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGAT
TTTATCAAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAA
GATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGGAAAATATTGAACCT
AGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTGAAGATTTACTTAAGAACGAGAACA
CAGGCAGCCGATCTATTAGTTAAAAGTTGCACTCAAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7302
STRAIN 090
TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTATTT
AGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTGAACGTGAAA
CTTTCCAACAGTCTTTTCAGCAAcTAATGACCGAACTATcTGATGTATAT
GGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTTCA
AGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGACCATATTC
AACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGtACAGGAAAC
ATTATAACATCCATCAATTTAAATGAAAGTATCGGTGCTGATGGTCCTGC
CTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAAAAATGATT
ATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACCAAAACCTT
GAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATCAAGTCAAA
ATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGATA
ATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGGAAAATATT
GAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTGAAGATTTA
CTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAGTTGCACTC
AAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7303
STRAIN A909
TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTAT
TTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTGAACGTGA
AACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTGATGTAT
ATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTT
CAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGACCATAT
TCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGTACAGGAA
ACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGATGGTCCT
GCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAAAAATGA
TTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACCAAAACC
TTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATCAAGTCA
AAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGA
TAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGGAAAATA
TTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTGAAGATT
TACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAGTTGCAC
TCAAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7304
STRAIN H36B
TCTGCTATAATAGACAAAAAGGTGGTGATATTT
ATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTGA
ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
GAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGA
CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGTA
CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
GGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAA
AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC
AAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATC
AAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGG
AAAATATTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTG
AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAG
TTGCACTCAAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7305

SEQUENCE LISTING

STRAIN 18RS21
TCTGCTATAATAGACAAAAAGGTGGTGATATTT
ATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTGA
ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
GAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGA
CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGTA
CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
GGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAA
AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC
AAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATC
AAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGG
AAAATATTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTG
AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAG
TTGCACTCAAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7306
STRAIN M732
TCTGCTATAATAGACAAAAAGGTGGTGATATT
TATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTG
AACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
TGAATTTCAAGCTTTATTGAAACaATCAAAAAAGGTATTTCAAATTATTG
ACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGT
ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
TGGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATA
AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
CAAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTAT
CAAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATAC
TTCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTG
GAAAATATTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCT
GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAA
GTTGCACTCAAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7307
STRAIN COH1
TCTGCTATAATAGACAAAAAGGTGGTGATATT
TATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTG
AACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
TGAATTTCAAGCTTTATTGAAACaATCAAAAAAGGTATTTCAAATTATTG
ACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGT
ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
TGGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATA
AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
CAAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTAT
CAAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATAC
TTCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTG
GAAAATATTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCT
GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAA
GTTGCACTCAAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7308
STRAIN M781
TCTGCTATAATAGACAAAAAGGTGGTGATATTT
ATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTGA
ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
GAATTTCAAGCTTTATTGAAACAATCAAAAAAGGTATTTCAAATTATTGA
CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGTA
CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
GGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAA
AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC

SEQUENCE LISTING

AAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATC
AAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGG
AAAATATTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTG
AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAG
TTGCACTCAAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7309
STRAIN CJB110
TCTGCTATAATAGACAAAAAGGTGGTGGTA
TTTATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACT
TGAACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTAT
CTGATGTATATGGTGAAGAGCTGATTTCTCTATTCACTATTACAGCTGGT
GATGAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTAT
TGACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCG
GTACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCT
GATGGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGA
TAAAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAG
ACCAAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTT
ATCAAGTCAAAATGGACTACTAACCATTTTCAAATGCTTGAGCACTTAAT
ACTTCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAAC
TGGAAAATATTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGT
CTGAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAA
AAGTTGCACTCAAACTAAAGGGGGAAGCTATGATTTc

SEQ ID NO. 7310
STRAIN JM9130013
TCTGCTATAATAGACAAAAAGGTGGTGATATTT
ATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTGA
ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
GAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGA
CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGTA
CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
GGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAA
AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC
AAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATC
AAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGG
AAAATATTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTG
AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAG
TTGCACTCAAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7311
STRAIN 2603 frame: 1
LSAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITA
GDEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHAR
SAINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQ
DNYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7312
STRAIN 090 frame: 1
SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINLNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7313
STRAIN A909 frame: 1
SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQUENCE LISTING

SEQ ID NO. 7314
STRAIN H36B frame: 1
SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7315
STRAIN 18RS21 frame: 1
SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7316
STRAIN M732 frame: 1
SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
DEFQALLKQSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7317
STRAIN COH1 frame: 1
SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
DEFQALLKQSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7318
STRAIN M781 frame: 1
SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
DEFQALLKQSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7319
STRAIN CJB110 frame: 1
SAIIDKKVVVFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISLFTITAG
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7320
STRAIN JM9130013 frame: 1
SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7401
STRAIN 2603
ATGGAAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATTACGGAACACTCTAT
CTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGGATTTTA
AGAGAAGTTGATTTTATTTGTGCAGAGGATACACGAAATACGGGACTTTTACTCAAGCAC
TTTGATATTACTACTAAACAAATTAGTTTTCACGAACACAATGCTTACGATAAAATCTCT
GGGTTAATTGATTTGTTAAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATG
CCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
GTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGGTTTAGCT
CCACAACCTCATATTTTTTATGGCTTCTTACCTCGTAAGAAAGGTCAACAAATAACTTTC
TTTGAAACAAAGCAAGATTACCCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGTC
TCTGATACGCTAAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGC
GAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGAGCAT
ATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAGAGAGATACC
GAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAGTATTAGTAAAAGAATATATCGCT

AATGGTGATAAAACTAATCAAGCGATAAAAAAAGTAGCAAAAGAATTTAATCTCAATAGA
CAAGAACTCTATGCTAGTTTCCATGATTTA

SEQ ID NO. 7402
STRAIN 090
GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATTACGGGACACT
CTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTG
CCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACGA
AATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAG
TTTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGT
TAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCT
ATTTCTGACCCAGgACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGAT
CCCGGTCGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCG
CTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCGCGT
AAGAAAGGTCAACAAATAACTTTTTTTGAAACAAAGAAAGATTACCCTGa
AACACAAATCTTTTATGAGTCACCGtTTCGAGTCTcTGATACGCTAAAAC
ACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGCGAATTG
ACGAAaCTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGG
GCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATG
GTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTA
GTATTAGTAA

SEQ ID NO. 7403
STRAIN A909
AGTTCAAAAAAGTTTTAAATCAAATATACATTACGGAACACTCTATCTAG
TCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGG
ATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACGAAATACGGG
ACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAGTTTTCACG
AACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGTTAAAAGAA
GGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATTTCTGA
CCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCAGTTG
TATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGGT
TTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCACGTAAGAAAGG
TCAACAAATAACTTTCTTTgAAACAAAGCAAGATTACCCTGAAACACAAA
TCTTTTATGAGTCACCGTTTCGAGTCTCtGATACGCTAAAACACATGAAA
GAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGCGAATTGACGAAACT
CTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGAGCATATTG
AAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAGAGA
GATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAGTATTAGT
AA

SEQ ID NO. 7404
STRAIN H36B
GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATT
ACGGGACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATG
ACTTTTCGTGCCATTAGGATTTTAAGAgAAGTTGATTTTATTTGTGCAGA
GGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTCACGAACACAATGCTTATGATAAAATCTCTGGGTTA
ATTGATTTGTTAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGG
AATGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
AAGGGGATATCCCGGTCGTATCTATACCAGGAGCTAGCGCTGGTATTACT
GCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTT
CTTACCGCGTAAGCAAGGTCAACAAATAACTTTTTTTGAAACAAAGAAAG
ATTACCCTGAAACACAAATCTTTTATGAGTCACCGtTTCGAGTCTCTGAT
ACGCTAAAACACATGAAAGAGATTTATGGAGATCGCCAAGTTGTTTTAGT
ACGCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTC
AACTTTTAGGGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATT
ATTGTTGATGGTAAGAGAGATACTGAGCGAGTGAAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7405
STRAIN 18RS21
GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATT
ACGGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAgATGATATG

SEQUENCE LISTING

ACTTTtCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGA
GgATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTA
ATTGATTTGTTAAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGG
AATGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
AAGGGGATATCCCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACT
GCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTT
CTTACCACGTAAGAAAGGTCAACAAATAACTTTCtTTGAAACAAAGCAAG
ATTACCCTGAAACACAAATCTTTTATGAGTCACCGtTTCGAGTCTCTGAT
ACGCTAAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGT
ACGCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTC
AACTTTTAGAGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATT
ATTGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7406
STRAIN M732
GAAATGCAAGTTCAAAAAAGTTTTAAATCAAAT
ATACATTACGGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGA
TGATATGACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTT
GTGCAGAGGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATT
ACTACTAAACAAATTAGTTTTCACGAACACAATGCTTACGATAAAATCTC
TGGGTTAATTGATTTGTTAAAAGAAGGGAAATCTTTAGCCCAAGTATCTG
ATGCAGGAATGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCT
GCTATTGAAGGGGATATCCCAGTTGTATCTATACCAGGAGCTAGCGCTGG
TATTACTGCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTT
ATGGCTTCTTACCACGTAAGAAAGGTCAACAAATAACTTTCTTTGAAACA
AAGCAAGATTACCCTGAAACACAAATCTTTTATGAGTCACCGtTTCGAGT
CTCTGATACGCTAAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTG
TTTTAGTACGCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACC
ATTAGTCAACTTTTAGAGCATATTGAAAAGGTCCCTCTCAAAGGTGAATG
CTTAATTATTGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTA
GCCAACAAGATCCACTAGTATTAGTAA

SEQ ID NO. 7407
STRAIN COH1
GAAATGCAAGTTCAAAAAAGTTTTaAATCAAATATACATTAC
GGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGAC
TTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGG
ATACACGAAATACGGGAcTTTTACTCAAGCACTTTGATATTACTACTAAA
CAAATTAGTTTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTAAT
TGATTTGTTAAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAA
TGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAA
GGGGATATCCCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGC
TCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCT
TACCACGTAAGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAGAT
TACCCTGAAACACAAATCTTTTATGAGTCACCGtTTCGAGTCTCTGATAC
GCTAAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTAC
GCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAA
CTTTTAGAGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTAT
TGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAG
ATCCACTAGTATTAGTAA

SEQ ID NO. 7408
STRAIN M781
AAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATTACGGAACACTC
TATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGC
CATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACGAA
ATACGGgACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAGT
TTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGTT
AAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTcTA
TTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATC
CCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGC
TTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCACGTA

SEQUENCE LISTING

AGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAGATTACCCTGAA
ACACAAATCTTTTATGAGTCACCGTTTCGAGTcTcTGATACGCTAAAACA
CATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGCGAATTGA
CGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGAG
CATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGG
TAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAG
TATTAGTAA
A

SEQ ID NO. 7409
STRAIN CJB110
GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATTACGGGACAC
TCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGT
GCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACG
AAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTA
GTTTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTG
TTAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTC
TATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGA
TCCCGGTCGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATC
GCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCGCG
TAAGAAAGGTCAACAAATAACTTTTtTTTGAAACAAAGAAAGATTACCCTG
AAACACAAATCTTtTTATGAGTCACCGtTTcGAGTCTCTGATACGCTAAAA
CACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGCGAATT
GACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAG
GGCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGAT
GGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACT
AGTATTAGTAA

SEQ ID NO. 7410
STRAIN 1169NT
TGCAAGTTCAAAAAAGTTTTAAATCAAATACACATTATGGGACACTCTAT
CTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCAT
TAGGATTTTAAGAgAAGTTGaTTTTATTTGTGCAGAGGATACACGAAATA
CGGGACTTTTACTCAAGCACTTTGATaTTACTACTAAACAAATTAGtTTT
cACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTtGTTAAA
AGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATTT
CTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
GTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTC
AGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCACGTAAGA
AAGGTCAACAAATAACTTTTTTTGAAACAAAGCAAGATTATCCTGAAACA
CAAATCTTTTATGAGTCACCGtTTCGAGTCTCTGATACGCTAAAACACAT
GAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGCGAATTGACgA
AACTCTATGAAGAGTATCAAAGAGGAACCATTaGTCAACTTTTAGAGCAT
ATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGtTGATGGTAA
GAGAGAtaCCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAGTAT
TAGTAA

SEQ ID NO. 7411
STRAIN JM9130013
GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATTACGGGA
CACTCTATCTAGTCCCAACTCCAATTGGTAATCTAgATGATATGACTTTT
CGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATAC
ACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAA
TTAGTTTTCACGAACACAATGCTTATGATAAAATCTCTGGGTTAATTGAT
TTGTTAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCC
CTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCtGCTATTGAAGGGG
ATATCCCGGTCGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTC
ATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACC
GCGTAAGCAAGGTCAACAAATAACtTTTTTTGAAACAAAGAAAGATTACC
CTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTA
AAACACATGAAAGAGATTTATGGAGATCGCCAAGTTGTTTTAGTACGCGA
ATTGACGAAACTCTATGAAGAGTATCAAaGAGGAACCATTAGTCAACTTT
TAGGGCATATTGaAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTT
GATGGTAAGAGAGATACTGAGCGAGTGAAAGACAGTAGCCAACAAGATCC

SEQUENCE LISTING

AGTAGTATTAGTAA

SEQ ID NO. 7412
STRAIN 2603 frame: 1
MEMQVQKSFKSNIHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
DITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAAIEGDIPV
VSIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVS
DTLKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTE
RVKDSSQQDPLVLVKEYIANGDKTNQAIKKVAKEFNLNRQELYASFHDL

SEQ ID NO. 7413
STRAIN 090 frame: 1
EMQVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAAIEGGIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKKDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLGHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7414
STRAIN A909 frame: 2
VQKSFKSNIHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDITT
KQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVVSIP
GASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDTLK
HMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTERVKD
SSQQDPLVLV

SEQ ID NO. 7415
STRAIN H36B frame: 1
EMQVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKQGQQITFFETKKDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLGHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7416
STRAIN 18RS21 frame: 1
EMQVQKSFKSNIHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7417
STRAIN M732 frame: 1
EMQVQKSFKSNIHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7418
STRAIN COH1 frame: 1
EMQVQKSFKSNIHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7419
STRAIN M781 frame: 3
MQVQKSFKSNIHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDI
TTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVVS
IPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDT
LKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTERV

KDSSQQDPLVLV

SEQ ID NO. 7420
STRAIN CJB110 frame: 1
EMQVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAAIEGGIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKKDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLGHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7421
STRAIN 1169NT frame: 3
QVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDIT
TKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVVSI
PGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDTL
KHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTERVK
DSSQQDPLVLV

SEQ ID NO. 7422
STRAIN JM9130013 frame: 1
EMQVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKQGQQITFFETKKDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLGHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPVVLV

SEQ ID NO. 7501
STRAIN 2603
ATGAGCGTATATGTTAGTGGAATAGGAATTATT
TCTTCTTTGGGAAAGAATTATAGCGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGA
ATTTCTAAACATTTATATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATA
ACTAGTGACCCAGAGGTTCCTGAGCAATACAAAGATGAGACACGTAATTTTAAATTTGCT
TTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAAAAGCTTATCATAAT
ATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAAAGAGTGCTGGTCAAAATGCCTTGTAT
CAATTTGAAGAAGGAGAGCGTCAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTAC
CATATTGCTGATGAATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCA
ACCGCCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGATGGC
GATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGATATTTCTTTAGCAGGC
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GGAATCAATTTGGGTGAGGGCGCTGGTTTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCT
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AAGCCAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGGTATT
GACTACAGTGAGATTGACTATATTAACGGTCACGGTACAGGTACTCAAGCTAATGATAAA
ATGGAAAAAAATATGTATGGTAAGTTTTTCCCGACAACGACATTGATCAGCAGTACCAAG
GGGCAAACGGGTCATACTCTAGGGGCTGCAGGTATTATCGAATTGATTAATTGTTTAGCG
GCAATAGAGGAACAGACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCA
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TTTGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTTTAGATTCACCTCTAGAA
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SEQ ID NO. 7506
STRAIN M732

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TTTGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7509
STRAIN CJB110
ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
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GGTTTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAAAAT
TATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGC
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GACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAA
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TCAGTTTGGATTTTCATCTAATGGTGCTGGTGAAGAACTGGACTATACTG
TTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTCGATC
TTTGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7510
STRAIN 1169NT
ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAG
CGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATT
TATATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAACT
AGTGACCCAGAGGTTCCTGAGCAATACAAAGATGAGACACGTAATTTTAA

SEQUENCE LISTING

ATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATT
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AGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATG
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AGATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTG
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CTCAAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTTTCCCG
ACAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCATACTCTAGG
GGCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAAC
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CTCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACA
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GTTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTCGAT
CTTTGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7511
STRAIN JM9130013
ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGCGAG
CATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTTATA
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ACCCAGAGGTTCCTGAGCAATACAAAGATGAGACACGTAATTTTAAATTT
GCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAAA
AGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAAAGA
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GATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGAATT
GATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCGCCT
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GGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGATAT
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CGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGCCAA
CAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGGT
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AGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTTTCCCGACAA
CGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCATACTCTAGGGGCT
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TGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAAATT

SEQUENCE LISTING

TTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAATTTT
TCGTTTGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTTTAGA
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ATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAAATAACAGGTCC
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TTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGGTCA
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GGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7512
STRAIN 2603 frame: 1
MSVYVSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQ
YKDETRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQV
DASLLEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGG
CDELSDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGL
ITSDGYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKF
FPTTTLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKR
EYPIRNALNFSFAFGGNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITY
EKVASNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTS
KVGIVFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSV
ISTNSGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSA
QVLSRQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNER
KKAVSSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIF
GGISFAIIEKR

SEQ ID NO. 7513
STRAIN 090 frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGILLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7514
STRAIN A909 frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI

SEQUENCE LISTING

RNALNFSFAFGGNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7515
STRAIN H36B frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7516
STRAIN 18RS21 frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7517
STRAIN M732 frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7518
STRAIN COH1 frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI

RNALNFSFAFGGNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7519
STRAIN M781 frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGILLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7520
STRAIN CJB110 frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGILLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7521
STRAIN 1169NT frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGILLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7522
STRAIN JM9130013 frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
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RNALNFSFAFGGNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
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FAIIEKR

SEQ ID NO. 7601
STRAIN 2603
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SEQ ID NO. 7602
STRAIN 090
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SEQ ID NO. 7603
STRAIN A909
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SEQ ID NO. 7604
STRAIN H36B
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SEQUENCE LISTING

ACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCA
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SEQ ID NO. 7605
STRAIN 18RS21
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SEQ ID NO. 7606
STRAIN M732
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SEQ ID NO. 7607
STRAIN COH1
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SEQUENCE LISTING

SEQ ID NO. 7608
STRAIN M781
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SEQ ID NO. 7609
STRAIN CJB110
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SEQ ID NO. 7610
STRAIN 1169NT
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SEQ ID NO. 7611
STRAIN JM9130013
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SEQUENCE LISTING

AGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTAC
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CTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7612
STRAIN 2603 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
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DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGHSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7613
STRAIN 090 frame: 3
LKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTALVLDT
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LDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKDEGRSI
FITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7614
STRAIN A909 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
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DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7615
STRAIN H36B frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7616
STRAIN 18RS21 frame: 1
DLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTALVLD
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QLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKDEGHS
IFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7617
STRAIN M732 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7618
STRAIN COH1 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7619
STRAIN M781 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQUENCE LISTING

SEQ ID NO. 7620
STRAIN CJB110 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
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DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7621
STRAIN 1169NT frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQQITHISKVV
DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7622
STRAIN JM9130013 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
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DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
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SEQ ID NO. 7701
STRAIN 2603
TTGCCTATGTTGTCTGTTGGTTTAGTTTTAGAGGGTGGCGGAATGAGAGGTCTTTATACT
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SEQ ID NO. 7702
STRAIN 090
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SEQ ID NO. 7703
STRAIN A909
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SEQUENCE LISTING

AGATGCAGGAATAAAAGTAGATGGTATCATATCTGTCTCTGCTGGTGCAT
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SEQ ID NO. 7704
STRAIN H36B
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SEQ ID NO. 7705
STRAIN 18RS21
CCTATGTTGTCTGTTGGTTTAGTTTTAGAGG
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TTCAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAATTTTG
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SEQ ID NO. 7706
STRAIN M732
CCTATGTTGTCTGTTGGTTTAGTTTTAGA
GGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTTC
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TTGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATA
CAATAAAAAGTATTTATCCCACCCTGAATATATGAGTCTAAGATCATGGC
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ATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGA
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CCTTCAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAATTT
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SEQ ID NO. 7707
STRAIN COH1
CCTATGTTGTCTGTTGGTTTAGTTTTA
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SEQ ID NO. 7708
STRAIN M781
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SEQ ID NO. 7709
STRAIN CJB110
CCTATGTTGTCTGTTGGTTTAGTTTTA
GAGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTT
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SEQUENCE LISTING

TACAATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATG
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SEQ ID NO. 7710
STRAIN 1169NT
CCTATGTTGTCTGTTGGTTTAGTTTTAGAGGGTG
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SEQ ID NO. 7711
STRAIN JM9130013
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GGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTTCT
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GGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCAAGTA
AGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGT
ATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTGAA
TAGTTATCTAATGAAA

SEQ ID NO. 7712
STRAIN 2603 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSHPKYMSLRSWFRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPELNSYLMK

SEQUENCE LISTING

SEQ ID NO. 7713
STRAIN 090 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSHPKYMSLRSWFRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPELNSYLMK

SEQ ID NO. 7714
STRAIN A909 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKVDGIISVSAGALFGVNFVSRQRERALRY
NKKYLSHPKYMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYAVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVVWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7715
STRAIN H36B frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKVDGIISVSAGALFGVNFVSRQRERALRY
NKKYLSHPKYMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYAVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVVWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7716
STRAIN 18RS21 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSHPKYMSLRSWFRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPELNSYLMK

SEQ ID NO. 7717
STRAIN M732 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSHPEYMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKYAKSVMPELNSYLMK

SEQ ID NO. 7718
STRAIN COH1 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSHPEYMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKYAKSVMPELNSYLMK

SEQ ID NO. 7719
STRAIN M781 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSHPEYMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKYAKSVMPELNSYLMK

SEQ ID NO. 7720
STRAIN CJB110 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSHPKYMSLRSWFRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPELNSYLMK

SEQUENCE LISTING

SEQ ID NO. 7721
STRAIN JM9130013 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKVDGIISVSAGALFGVNFVSRQRERALRY
NKKYLSHPKYMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYAVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVVWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7722
STRAIN 1169NT frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
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GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
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SEQ ID NO. 7801
STRAIN 2603
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GGCATATCTACC

SEQ ID NO. 7802
STRAIN 090
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CAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7803
STRAIN A909
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SEQUENCE LISTING

ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTGCACCGCTCTT
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SEQ ID NO. 7804
STRAIN H36B
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SEQ ID NO. 7805
STRAIN 18RS21
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SEQ ID NO. 7806
STRAIN M732
AAAGTTTTAGTAGTTGATGATGAACCAGTT
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TTTAACCAAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGT
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SEQ ID NO. 7807
STRAIN COH1
AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTA
ACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCA
GAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAAACTTT

SEQUENCE LISTING

TGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAAT
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AAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGA
GCAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7808
STRAIN M781
AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTAAC
GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
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SEQ ID NO. 7809
STRAIN CJB110
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CTTTGTAATAAAATAACAGTTCCTGTTAGCAGAGCAAATGTAAAACCCCT
AAAACAAATGTTAGG

SEQ ID NO. 7810
STRAIN 1169NT
AAAGTTTTAGTAGTTGATGATGAACCAG
TTGCACGTAACGAATTAATTTATCTTCTTAATAAGTATGATTCTAACCTC
GTTATAGCAGAGGCGCATGATATAGCTACTGCATTAGCTATTTTACTTAG
AGAAACTTTTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTG
GGTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTATTG
ATATTCGCGACTGCTTATGATCAATATGCTATTCAGGCTTTTGAGCATGA
TGCGCGTGATTATTTGTTAAAACCCTATGAGTTTGATAGGCTAAAGCAAG
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TCGAATCTATCTGGTGTCGGCGGATGATATCCTTTTGATTGAAGCTATGC
AAGGAAAACTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGC
TCTCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGT
GCACCGCTCTTACATTGTGAATATTAATGCTATTAAAACGATTGAACCTT
GGTTTAACCAAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCT

SEQUENCE LISTING

GTTAGCAGAGCAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTAC
C

SEQ ID NO. 7811
STRAIN JM9130013
AAAGTTTTAGTAGTTGATGATGAACCAGT
TGCACGTAACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCG
TTATAGCAGAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGA
GAAACTTTTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGG
GTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGA
TATTCGCGACTGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGAT
GCGCGTGATTATTTGTTAAAACCCTATGAGTTTGATAGGCTAAAGCAAGC
TATGGATAGAGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCG
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CGAATCTATCTGGTGTCGGCGGATGATATCCTTTTGATTGAAGCTATGCA
AGGAAAACTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCT
CTCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTG
CACCGCTCTTACATTGTGAATATTAATGCTATTAAAACGATTGAACCTTG
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TTAGCAGAGCAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7812
STRAIN 2603 frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7813
STRAIN 090 frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7814
STRAIN A909 frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7815
STRAIN H36B frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7816
STRAIN 18RS21 frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7817
STRAIN M732 frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG

SEQUENCE LISTING

LQLAEYINKMPKPPLLIFATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVASGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7818
STRAIN COH1 frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVASGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7819
STRAIN M781 frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVASGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7820
STRAIN CJB110 frame: 1
LNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSGLQLAEYINKMPKPPLLIF
ATAYDQYAIQAFEHDARDYLLKPYEFDRLKQXMDRVKGALSTSTIIESVTSGPLFKQQYP
LTVEDXIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQWQDKLPSSQFVRVHRSYI
VNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQML

SEQ ID NO. 7821
STRAIN 1169NT frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDIATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7822
STRAIN JM9130013 frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7901
STRAIN 2603
ATGGGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCCGGCACTCCTTTTGAAGGG
CGTGCCCTTTTTGACGTCAATCTGAAAATTGAAGATGCTTCCTATACCGCGTTCATTGGG
CACACAGGTTCTGGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACA
AAAGGTGAGGTAATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACAAAGAAATC
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GCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGA
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GGGAAAGTAACCTTATCAGGACAACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAA
AGTAAACAATTAGGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGA
TTAAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7902
STRAIN 090
GGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC

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AGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCTGGAAAATCAA
CTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAAAGGTGAGGTA
ATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACAAAGAAATCAA
ATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCAGAAAGTCAGC
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AGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTTGAACTTTCTG
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AAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAAGGAATGACTA
TCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTAT
GTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAAACA
GATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTAGGAGTTCCCA
AAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATTAAATTTACCT
AGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7903
STRAIN A909
GGAATTGAATTTAAAAATGTAAGTTATACCTATCAA
GCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTTGACGTCAATCTGAAAAT
TGAAGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCTGGAAAAT
CAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAAAGGTGAG
GTAATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACAAAGAAAT
CAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCAGAAAGTC
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CTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGCGATGGAA
CCCAAAGTACTAGTACTAGATGAGCCAACAGCTGGACTTGATCCTAAGGG
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CTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGAC
TATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAA
GCAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTAGGAGTTC
CCAAAATCACCAAGTTTGCTCAAAGGCTATCTCATAAGGGATTAAATTTA
CCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTAAGCATGG
A

SEQ ID NO. 7904
STRAIN H36B
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CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTTGACGTCAATC
TGAAAATTGAAGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCT
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AGGTGAGGTAATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACA
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AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
GATGGAACCCAAAGTACTAGTACTAGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
AACCAAAGCAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
GGAGTTCCCAAAATCACCAAGTTTGCTCAAAGGCTATCTCATAAGGGATT
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AGCATGGA

SEQ ID NO. 7905
STRAIN 18RS21
GGAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTTGACGTCAATC
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GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAA
AGGTGAGGTAATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACA
AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCA
GAAAGTCAGCTTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACC
ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
AACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
GGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7906
STRAIN M732
GGAATTGAATTTAAAAATGTAAGTTATAC
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AGGTGAGGTAATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACA
AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCA
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ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
AACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
GGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7907
STRAIN COH1
GGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC
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CTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAAAGGTGAGGTA
ATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACAAAGAAATCAA
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GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGCGATGGAACCC
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GATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTAGGAGTTCCCA
AAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATTAAATTTACCT
AGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7908
STRAIN M781
GGAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTTGACGTCAATC
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GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAA
AGGTGAGGTAATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACA

SEQUENCE LISTING

AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCA
GAAAGTCAGCTTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACC
ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
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CTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
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AACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
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AGCATGGA

SEQ ID NO. 7909
STRAIN CJB110
GGAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTTGACGTCAATC
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GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
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GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
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AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7910
STRAIN 1169NT
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GTTATACCTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTTGAC
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AGGTTCTGGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTC
CTACAAAAGGTGAGGTAATTGTCGATGATTTTTCTATTAAAGCAGGGGAC
AAGAACAAAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCA
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TCCATTTGAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTA
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CTTGATCCTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCA
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CGGATTATGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTA
TCAGGACAACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAA
ACAATTAGGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATA
AGGGATTAAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAG
GCTATTAAGCATGGA

SEQ ID NO. 7911
STRAIN JM9130013
GGAATTGAATTTAAAAATGTAAGTT
ATACCTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTTGACGTT
AATCTGAAAATTGAAGATGCTTCCTATACCGCATTCATTGGGCACACAGG
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CAAAAGGTGAGGTAATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAG
AACAAAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATT

SEQUENCE LISTING

TCCAGAAAGTCAGCTTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTG
GACCACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAA
GAAAAATTAAGGTTAGTTGGTATTAGTGAGGATTTATTCGATAAAAATCC
ATTTGAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTT
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AAAAGGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGG
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GGACAACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACA
ATTAGGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGG
GATTAAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCT
ATTAAGCATGGA

SEQ ID NO. 7912
STRAIN 2603 frame: 1
MGIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7913
STRAIN 090 frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7914
STRAIN 090 frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7915
STRAIN H36B frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7916
STRAIN 18RS21 frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7917
STRAIN M732 frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7918
STRAIN COH1 frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK

SEQUENCE LISTING

GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7919
STRAIN M781 frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7920
STRAIN CJB110 frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7921
STRAIN 1169NT frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7922
STRAIN JM9130013 frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 8001
STRAIN 2603
GTGAACCACTTACTTAACCTCAGTAAAGAAAATATAGCTAAAATAGATTTTGACTTTCTT
AATGAGGCACTTAATGCAAATATTCGTTTGAAAGAATTAGTAGATGAACTAAAAATTTCA
AAAGAACTGGACAGTAAAGGTTGGTCCAAAAAAGACTCTCGAACGATAAAAATCTTGTAC
GATGGCCTTATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCAA
GTCATTCCATTTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAAGGGAGAATTCT
AAAAATTATAGAATATACAACTACAGTGATTATGAAATGGAGTTAATCAATGAGGATAGG
CAACAATTTTCAAAATATGAAACAGTTGATTTAGACCAATTGATACTTGTTGATATTTTT
AATATTGATGACTACATTTCATCATATTTAACAATA

SEQ ID NO. 8002
STRAIN H36B
AACCACTTACTTAACCTCAGTAAAGAAAATATAGCT
AAAATAGATTTTGACTTTCTTAATGAGGCACTTAATGCAAATATTCGTTT
GAAAGAATTAGTAGATGAACTAAAAATTTCAAAAGAACTGGACAGTAAAG
GTTGGTCCAAAAAAGACTCTCGAACGATAAAAATCTTGTACGATGGCCTT
ATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCA
AGTCATTCCATTTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAA
GGGAGAATTCTAAAAATTATAgAATATACAACTACAGTGATTATGAAATG
GAGTTAATCAATGAGGATAGGCAACAATTTTCAAAATATGAAACAGTTGA
TTTAGACCAATTGATACTTGTTGATATTTTTAATATTGATGACTACATTT
CATCATATTTAACAATA

SEQ ID NO. 8003
STRAIN 18RS21
AACCACTTACTTAACCTCAGTAAAGAAAATATAG

CTAAAATAGATTTTGACTTTCTTAATGAGGCACTTAATGCAAATATTCGT
TTGAAAGAATTAGTAGATGAACTAAAAATTTCAAAAGAACTGGACAGTAA
AGGTTGGTCCAAAAAAGACTCTCGAACGATAAAAATCTTGTACGATGGCC
TTATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATC
CAAGTCATTCCATTTGCTAATGTACATGTACTACTGTTTTTAATACCAGA
AAGGGAGAATTCTAAAAATTATAGAATATACAACTACAGTGATTATGAAA
TGGAGTTAATCAATGAGGATAGGCAACAATTTTCAAAATATGAAACAGTT
GATTTAGACCAATTGATACTTGTTGATATTTTTAATATTGATGACTACAT
TTCATCATATTTAACAATA

SEQ ID NO. 8004
STRAIN 2603 frame: 1
VNHLLNLSKENIAKIDFDFLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILY
DGLINKHIVSLDRADYNIIQVIPFANVHVLLFLIPERENSKNYRIYNYSDYEMELINEDR
QQFSKYETVDLDQLILVDIFNIDDYISSYLTI

SEQ ID NO. 8005
STRAIN H36B frame: 1
NHLLNLSKENIAKIDFDFLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILYD
GLINKHIVSLDRADYNIIQVIPFANVHVLLFLIPERENSKNYRIYNYSDYEMELINEDRQ
QFSKYETVDLDQLILVDIFNIDDYISSYLTI

SEQ ID NO. 8006
STRAIN 18RS21 frame: 1
NHLLNLSKENIAKIDFDFLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILYD
GLINKHIVSLDRADYNIIQVIPFANVHVLLFLIPERENSKNYRIYNYSDYEMELINEDRQ
QFSKYETVDLDQLILVDIFNIDDYISSYLTI

SEQ ID NO. 8101
STRAIN 090
AGCAAGCCTAATGTTGTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTCATG
CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
TAACTAATAGAACTGAGAACCAGAAGTTGCTAGCAAAACAACTAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
CGGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8102
STRAIN A909
AGCAAGCCTAATGTTGTTCAGTTAAATAATCAATA
TATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCG
TTTAATGGGTTGGGTTCTTATTTTTGTCATGCTTtttATTTATTTTACCCACTTATAATTT
AGTTAAGAGTTACAGAACTTTACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGA
CTATCAGACATTAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACTAAAAAA
TCCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGACCGGCGAAAT
GATTTACCCATTACCAGACCT

SEQ ID NO. 8103
STRAIN H36B
AGCAAGCCTAATGTTGTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTCATG
CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACTAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
CGGCGAAATGATTTACCCATTACCAGACCtTTTACCAAAA

SEQ ID NO. 8104
STRAIN 18RS21
AGCAAGCCTAATGTTGTTCAGTTAAATAATCAATATATTAACGATGAGAATCTAAAAAAA
CGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTT

SEQUENCE LISTING

GTCATGCTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTTACAA
GAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACATTAACTAATAGAACT
GAGAACCAGAAGTTGCTAGCAAAACAACTAAAAAATCCAGATTACGTTCAAAAATATGCT
CGAGCTAAGTATTATTTCTCTAAGACCGGCGAAATGATTTACCCATTACCAGACCTTTTA
CCAAAA

SEQ ID NO. 8105
STRAIN M732
AGCAAGCCTAATGTTGTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTCATG
CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACTAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGAC
CGGCGAAATGATTTACCCATTACCAGACCtTTTACCAAAA

SEQ ID NO. 8106
STRAIN COH1
AGCAAGCCTAATGTTGTTCAGTTAAATAATC
AATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGGAGTTA
CGCCGAAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTCATGCTttt
ATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTTACAAG
AACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACATTAACT
AATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACTAAAAAATCCAGA
TTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGACCGGCG
AAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8107
STRAIN M781
AGCaAGCCTAATGTTGTTCAGTT
AAATAATCAATATaTTAACGATGAGAATCTAAAAAAACGTTACGAAGCTG
AGGAGTTACGCCGAAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTC
ATGCTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAAC
TTTACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGA
CATTAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACTAAAA
AATCCAGATTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAA
GACCGGCGAAATGATTTACCCATTACCAGACCtTTTACCAAAA

SEQ ID NO. 8108
STRAIN CJB110
AGCAAGCCTAATGTTGTTCAGTTAAATAATC
AATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGGAGTTA
CGCCGAAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTCATGCTttt
ATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTTACAAG
AACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACATTAACT
AATAGAACTGAGAACCAGAAGTTGCTAGCAAAACAACTAAAAAATCCAGA
TTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGACCGGCG
AAATGATTTACCCATTACCAGACCtTTTACCAAAA

SEQ ID NO. 8109
STRAIN 1169NT
AGCAAGCCTAATGTTGTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTCATG
CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACTAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
CGGCGAAATGATTTACCCATTACCAGACCtTTTACCAAAA

SEQ ID NO. 8110
STRAIN JM9130013
AGCaAGCCTAATGTTGTTCAGTTAAA

SEQUENCE LISTING

TAATCAATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTCATG
CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACTAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGAC
TGGCGAAATGATTTACCCATTACCAGACCtTTTACCAAAA

SEQ ID NO. 8111
STRAIN 2603
agcaagcctaatgttgttcagttaaataatcaatatattaacgatgagaa
tctaaaaaaacgttacgaagctgaggagttacgccgaaaaaatcgtttaa
tgggttgggttcttatttttgtcatgcttttatttattttacccacttat
aatttagttaagagttacagaactttacaagaacgtcgtcaagaagttgt
aaaattaacgaaagactatcagacattaactaatagaactgagaaccaga
agttgctagcaaaacaactaaaaaatccagattacgttcaaaaatatgct
cgagctaagtattatttctctaagaccggcgaaatgatttacccattacc
agaccttttaccaaaa

SEQ ID NO. 8112
STRAIN 090
SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
VKSYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
IYPLPDLLPK

SEQ ID NO. 8113
STRAIN A909
SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
VKSYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
IYPLPD

SEQ ID NO. 8114
STRAIN H36B
SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
VKSYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
IYPLPDLLPK

SEQ ID NO. 8115
STRAIN 18RS21
SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNLVKSYRTLQ
ERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEMIYPLPDLL
PK

SEQ ID NO. 8116
STRAIN M732
SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
VKSYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
IYPLPDLLPK

SEQ ID NO. 8117
STRAIN COH1
SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNLVK
SYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEMIY
PLPDLLPK

SEQ ID NO. 8118
STRAIN M781
SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYN
LVKSYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGE
MIYPLPDLLPK

SEQ ID NO. 8119
STRAIN CJB110
SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNLVK

SEQUENCE LISTING

SYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEMIY
PLPDLLPK

SEQ ID NO. 8120
STRAIN 1169NT
SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
VKSYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
IYPLPDLLPK

SEQ ID NO. 8121
STRAIN JM9130013
SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
VKSYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
IYPLPDLLPK

SEQ ID NO. 8122
STRAIN 2603
SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNLVKSYRTLQ
ERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEMIYPLPDLL
PK

SEQ ID NO. 8201
STRAIN 2603
ATGAAAAATTTATTGTTAAAATGTAAGGATAAGAAGGTTAAAGCATTTACACTTTTAGAA
TGTTTGGTAGCATTGGTTACAATCACAGGAGCTTTACTAGTTTATCAAGGACTGACAAAA
TTGTTGGCTCAACAGATAGTAGTGATGTCTTCTTCCAGTCAGTCTGAATGGGTGTTATTA
AcTCAGCAACTAAATGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAA
CTTTATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTTC
CGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAGACAATTGT
CAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTTTTTTATTTTAAGGACGGGTTAAAA
AGGACATTTTACTATGATTTTAAAGAAGAAACTTAA

SEQ ID NO. 8202
STRAIN 090
AATTCGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTATTTA
CGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTT
CCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGT
TAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACTTGTTTTT
TATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGA
AACT

SEQ ID NO. 8203
STRAIN A909
CAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAACTTTAT
TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
TTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATG
GGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTT
TTTTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGA
AGAAACT

SEQ ID NO. 8204
STRAIN H36B
ATGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAACTT
TATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGA
TGATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTT
ATGGGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTT
GTTTTTTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAA
AGAAGAAACT

SEQ ID NO. 8205
STRAIN 18RS21
AGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAACTTTATT
TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
TTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGG

GTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTTT
TTTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAA
GAAACT

SEQ ID NO. 8206
STRAIN M732
CAGAATTCGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTAT
TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
TTTCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATG
GGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTT
TTTTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGA
AGAAACT

SEQ ID NO. 8207
STRAIN COH1
GAATTCGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTATTT
ACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
TCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATGGG
TTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTTTT
TTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAG
AAACT

SEQ ID NO. 8208
STRAIN M781
AGAATTCGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTATT
TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
TTCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATGG
GTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTTT
TTTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAA
GAAACT

SEQ ID NO. 8209
STRAIN CJB110
GAATTCGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTATTT
ACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
TCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGG
TTAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACTTGTTTT
TTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAG
AAACT

SEQ ID NO. 8210
STRAIN 1169NT
TCGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTATTTACGT
AAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTTTCG
TAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAG
ACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACTTGTTTTTTAT
TTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGAAAC
T

SEQ ID NO. 8211
STRAIN JM9130013
TGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAACTTT
ATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGAT
GATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTA
TGGGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTG
TTTTTTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAA
GAAGAAACT

SEQ ID NO. 8212
STRAIN 2603 frame: 1
MKNLLLKCKDKKVKAFTLLECLVALVTITGALLVYQGLTKLLAQQIVVMSSSSQSEWVLL
TQQLNAEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNC
QMSQTKSMVKLVFYFKDGLKRTFYYDFKEET.

SEQUENCE LISTING

SEQ ID NO. 8213
STRAIN 090 frame: 3
FEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKS
MVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8214
STRAIN A909 frame: 3
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8215
STRAIN H36B frame: 3
AEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQT
KSMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8216
STRAIN 18RS21 frame: 2
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8217
STRAIN M732 frame: 3
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8218
STRAIN COH1 frame: 1
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8219
STRAIN M781 frame: 2
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8220
STRAIN CJB110 frame: 1
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8221
STRAIN 1169NT frame: 3
EGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKSM
VKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8222
STRAIN JM9130013 frame: 2
AEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQT
KSMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8301
STRAIN 2603
atgaaaaagattcgattatcaaagtttattaaaatgattgttgttattttgtttttaatt
agtgtagcagctagtttttatttttttccacgttgcccaagttcgagatgataaatccttt
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aagctattaaagcaaaaaatagaaatgacaaaccaaaatataaagcaagttgcttggtat
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cgcgagaacattatcaaatggacagaaatgatagttgataagaatccatcaagccaaatt
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cctagtcaggttgttaatatcattgaagattgcggttattctagtgtttgggatgaatta
aaatttcaggctaaagagatgtatggtttaccagccttcccactcttatatgaagtttca
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SEQUENCE LISTING

aaaaagaataatttaccagccctctttattcatggtgataaggataattttgttccaaca
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ggggcaaaacatgcgaaatcttttgaaacagagccagaaaaatatgagaaacgtatctct
agtttttgaaaaaatatgaaaaa

SEQ ID NO. 8302
STRAIN 090
GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCG
AGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
TATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
ATGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGCTAA
GAAAACTCATAAGACAGCTGTTGTCGTTCATGGTTTTGCGAATAgCAAAG
AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
cTTATGCCTGACAATATTGCACATGGtGAAAGTCATGGGCAGTTGATAGG
CTATGGCTGGAACGACCGCGAGAACATTATCaAATGGACAGAAATGATAG
TTGATAAGAATCCATCAAGCCAAATTACTTtaTTTGGTGTTTCAATGGGT
GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
TAATATCATTGAAGATTGCGGTTATTCTAGTGTTTGGGATGAATTAAAAT
TTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAA
GTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAG
TAGTGTCGAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATG
GTGATAAGGATAATTTTGTTCCAACAAGTATGGTTTATGACAACTATAAA
GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGC
GAAATCTTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8303
STRAIN A909
AATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTTATATGCT
TATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAATGACAAA
CCAAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGCTAAGAAAACTC
ATAAGACAGCTGTTGTCGTTCATGGTTTTGCGAATAGCAAAGAGAATATG
AAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTCTTATGCC
TGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGCTATGGCT
GGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGTTGATAAG
AATTCATCAAGCCAAATTACTTTATTTGGTGTTTCAATGGGTGGAGCAAC
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AACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATGGTGATAAG
GATAATTTTGTTCCAACAaGTATGGTTTATGACAACTATAAAGCTACAGC
AGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCGAAATCTT
TTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTTGAAA
AAATATGAAAAA

SEQ ID NO. 8304
STRAIN H36B
AGTTTTTATTTTTTCCACGTTGCCCAAGTTCGAGATGATAAATCCTTTAT
TTCAAATGGTCAACGTAAGCCTGGAAACTCTTTATATGCTTATGATAAAT
CCTTTGATAAGCTATTAAAGCAAAAAATAGAAATGACAAACCAAAATATA
AAGCAAGTTGCTTGGTATGTTCCTGCTGCTAAGAAAACTCATAAGACAGC
TGTTGTCGTTCATGGTTTTGCGAATAGCAAAGAGAATATGAAGGCATATG
GTTGGCTGTTTCATAAGTTAGGATACAATGTTcTTATGCCTGACAACATT
GCACATGGTGAAAGTCATGGGCAGTTGATAGGCTATGGCTGGAACGACCG
CGAGAACATTATCAAATGGACAGAAATGATAGTTGATAAGAATTCATCAA
GCCAAATTACTTTATTTGGTGTTTCAATGGGTGGAGCAACAGTCATGATG
GCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTAATATCATTGAAGATTG
CGGTTATTCtGGTGTTTGGGATGAATTAAAATTTCAGGCTAAAGAGATGT
ATGGTTTACCAGCCTTCCCACTCTTATATGAAGTTTCAACAATTTCTAAA
ATCAGAGCAGGTTTTTCGTATGGACAAgCAAGTAGTGTCGAACAATTGAA
AAAGAATAATTTACCAGCCCTCTTTATTCATGGTGATAAGGATAATTTTG
TTCCAACAAGTATGGTTTATGACAACTATAAAGCTACAGCAGGTAAGAAA
GAGCTTTATATTGTAAAAGGGGCAAAACATGCGAAATCTTTTGAAACAGA

SEQUENCE LISTING

GCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTGAAAAAaTATgAAA
AA

SEQ ID NO. 8305
STRAIN 18RS21
GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGA
GATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
ATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
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TTATGCCTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
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TGATAAGGATAATTTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
AAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
TTTGAAAAAATATGAAAAA

SEQ ID NO. 8306
STRAIN M732
GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGA
GATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
ATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
TGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGCTAAG
AAAACTCATAAGACAGTTGTTGTCGTTCATGGTTTTGCGAATAGCAAAGA
GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTC
TTATGCCTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
GGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTTCAATGGGTG
GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
AATATCATTGAAGATTGTGGTTATTCTAGTGTTTGGGATGAATTAAAATT
TCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAgCAAGT
AGTGTCGAACAATTGAAAAAGAATAATTTACCAGCCCTcTTTATTCATGG
TGATAAGGATAATTTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
AAATCTTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
TTTGAAAAAATATGAAAAA

SEQ ID NO. 8307
STRAIN COH1
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AATGaCAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGCTA
AGAAAACTCATAAGACAGTTGTTGTCGTTCATGGTTTTGCGAATAGCAAA
GAGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGT
TCTTATGCCTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAG
GCTATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATA
GTGGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTTCAATGGG
TGGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTG
TTAATATCATTGAAGATTGTGGTTATTcTAGTGTTTGGGATgAATTAAAA
TTTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGA
AGTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAA
GTAGTGTCGAACAATTGAAAAAGAATAATTTACCAGCCCTcTTTATTCAT
GGTGATAAGGATAATTTTGTTCCAACAaGTATGGTTTATGACAACTATAA
AGCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATG
CGAAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGT

SEQUENCE LISTING

TTTTTGAAAAAATATGAAAAA

SEQ ID NO. 8308
STRAIN M781
GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCG
AGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
TATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
ATGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGCTAA
GAAAACTCATAAGACAGTTGTTGTCGTTCATGGTTTTGCGAATAGCAAAG
AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
CTTATGCCTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
CTATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAG
TGGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTTCAATGGGT
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TAATATCATTGAAGATTGTGGTTATTcTAGTGTTTGGGATgAATTAAAAT
TTCAGGcTAAAGAGATGTATGGTTTACCAGCCTTCCCACTcTTATATGaA
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TAgTGTCGAACAATtGAAAAAGAATAATTTACCAGCCCTcTTTATTCATG
GTGATAAGGATAATTTTGTTCCAACAaGTATGGTTTATGaCAaCTATAAA
GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAGGGGCAAAACATGC
GAAATCTTTTGAAaCAGAGCCAGAaaAATATGAGAAACGTATCTCTAGTT
TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8309
STRAIN CJB110
GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGAG
ATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTTA
TATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAAT
GACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGCTAAGA
AAACTCATAAGACAGCTGTTGTCGTTCATGGTTTTGCGAATAGCAAAGAG
AATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTcT
TATGCCTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGCT
ATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGTT
GATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTTCAATGGGTGG
AGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTA
ATATCATTGAAGATTGCGGTTATTcTAGTGTTTGGGATgAATTAAAATTT
CAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAGT
TTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAgCAAGTA
gTGTCGAACAATTGAAAAAGAATAATTTACCAGCCCTcTTTATTCATGGT
GATAAGGATAATTTTGTTCCAACAAGTATGGTTTATGACAACTATAAAGC
TACAGCAGGTAAGAAAGAGCTTTATATTGTAAAGGGGCAAAACATGCGA
AATCTTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTT
TTGAAAAAATATGAAAAA

SEQ ID NO. 8310
STRAIN 1169NT
GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGA
GATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
ATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
TGACAAACCaAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGCTAAG
AAAACTCATAAGACAGCTGTTGTCGTTCATGGTTTTGCGAAtAGCAAAGA
gAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTc
TTATACCTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
TGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTTCAATGGGTG
GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
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TCAGGCTAaAGAGATGTATGGTTTaCCAGCCTTCCCACTcTTATATGAAG
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CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAGGGGCAAAACATGCG
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TTTGAAAAAATATGAAAAA

SEQUENCE LISTING

SEQ ID NO. 8311
STRAIN JM9130013
GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCG
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ATGaCAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGTTAA
GAAAACTCATAAGACAGCTGTTGTCGTTCATGGTTTTGCGAATAGCAAAG
AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
CTTATGCCTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
CTATGGCTGGAACGACCGCGAGAACATTATCaAATGGACAGAAATGATAG
TTGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTTCAATGGGT
GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
TAATATCATTGAAGATTGCGGTTATTcTAGTGTTTGGGATgAATTAAAAT
TTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAA
GTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAG
TAGTGTCGAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATG
GTGATAAGGATAATTTTGTTCCAACAAGTATGGTTTATGACAACTATAAA
GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGC
GAAATCTTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8312
STRAIN 2603 frame: 1
MKKIRLSKFIKMIVVILFLISVAASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFD
KLLKQKIEMTNQNIKQVAWYVPAVKKTHKTAVVVHGFANSKENMKAYGWLFHKLGYNVLM
PDNIAHGESHGQLIGYGWNDRENIIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKL
PSQVVNIIEDCGYSSVWDELKFQAKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQL
KKNNLPALFIHGDKDNFVPTSMVYDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRIS
SFLKKYEK

SEQ ID NO. 8313
STRAIN 090 frame: 1
ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
AKKTHKTAVVVHGFANSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8314
STRAIN A909 frame: 3
SFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPAAKKTHKTAVVVHGFA
NSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDRENIIKWTEMIVDKNSSS
QITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSGVWDELKFQAKEMYGLPAFPLLYE
VSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMVYDNYKATAGKKELYI
VKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8315
STRAIN H36B frame: 1
SFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPAA
KKTHKTAVVVHGFANSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDRENI
IKWTEMIVDKNSSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSGVWDELKFQA
KEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMVY
DNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8316
STRAIN 18RS21 frame: 1
ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
VKKTHKTAVVVHGFANSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8317

SEQUENCE LISTING

STRAIN M732 frame: 1
ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
AKKTHKTVVVVHGFANSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8318
STRAIN COH1 frame: 1
ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
AKKTHKTVVVVHGFANSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8319
STRAIN M781 frame: 1
ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
AKKTHKTVVVVHGFANSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8320
STRAIN CJB110 frame: 1
ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
AKKTHKTAVVVHGFANSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8321
STRAIN 1169NT frame: 1
ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
AKKTHKTAVVVHGFANSKENMKAYGWLFHKLGYNVLIPDNIAHGESHGQLIGYGWNDREN
IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8322
STRAIN JM9130013 frame: 1
ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
VKKTHKTAVVVHGFANSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8401
STRAIN 2603
ATGATGAAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACTAAAC
AATATGGAATGTTTAGCGACTGTCACTATCAATATCAAAAAGAATCATAGCATTAATTTG
ATGCCAGCCATTGATTTTTTAATGCAATCAATTGATTTAGAACCTCAAGATTTGGACCGT
ATCGTAGTAGCAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCA
AAAATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGCTTTA
ACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTATAGATGCACGACGTAATAAT
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TGTGCAGTAGCAATTGGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGTAGATGCGTTT
GTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTAAAAAACCACTGTGAA
ACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8402
STRAIN 090

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACT
AAACAATATGGAATGTTTAGCGACTGTCACTaTCAATATCAAAAAGAATC
ATAGCATTAATTTGATGCCAGCCATTGATTTTTTAATGCAATCAATTGAT
TTAGAACCTCAAGATTTGGACCGTATCGTAGTGGCAGAGGGTCCAGGATC
TTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAATGCTAGCTTATA
CGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGCTTTAACAAAT
GGATTTTCAGAAAATGATTTGTTGGTACCACTTATAGATGCACGACGTAA
CAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGTTAAACCAgACT
GTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGAATAAAGCCAAT
GTTCATTTTGTCGGAGAGGTTGCAGCATTTTTTGATCAGATTAAgAAAGC
CTTACCACATGCTAAAATTACAGAAACTTTACCTTGTGCAGTGGCAATTG
GGCGCAAAGGACAAAAAATGGAAAGCGTTAATGTAGATGCGTTTGTTCCA
CGATACTTAAAACGAGTTGAAGCTGAGGAAAATTGGTTAAAAAACCACTG
TGAAACGAAT

SEQ ID NO. 8403
STRAIN A909
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GTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAATG
CTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGC
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SEQ ID NO. 8404
STRAIN H36B
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SEQ ID NO. 8405
STRAIN 18RS21
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SEQ ID NO. 8406
STRAIN M732
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SEQ ID NO. 8407
STRAIN COH1
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SEQ ID NO. 8408
STRAIN M781
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SEQ ID NO. 8409
STRAIN CJB110
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SEQUENCE LISTING

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SEQ ID NO. 8410
STRAIN 1169NT
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SEQ ID NO. 8411
STRAIN JM9130013
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GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
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SEQ ID NO. 8412
STRAIN 2603 frame: 1
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VYVGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLP
CAVAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8413
STRAIN 090 frame: 1
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VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
VAIGRKGQKMESVNVDAFVPRYLKRVEAEENWLKNHCETN

SEQ ID NO. 8414
STRAIN A909 frame: 1
KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFVDQIKKVLPHAKITETLPCA
VAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLRNHCETN

SEQ ID NO. 8415
STRAIN H36B frame: 1
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VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFVDQIKKVLPHAKITETLPCA
VAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLRNHCETNTEEYIKRV

SEQ ID NO. 8416
STRAIN 18RS21 frame: 1
KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
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VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
VAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8417
STRAIN M732 frame: 1
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VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
VAIGRKGQKMKSVNVXXFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8418
STRAIN COH1 frame: 1
KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
VAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8419
STRAIN M781 frame: 1
KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VSEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
VAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8420
STRAIN CJB110 frame: 1
KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
VAIGRKGQKMESVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8421
STRAIN 1169NT frame: 1
KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
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VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFVDQIKKALPHAKITETLPCA
VAIGRKGQKMESVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8422
STRAIN JM9130013 frame: 1
KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
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VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFVDQIKKVLPHAKITETLPCA
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SEQ ID NO. 8501
STRAIN 2603
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SEQUENCE LISTING

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SEQ ID NO. 8502
STRAIN 090
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SEQ ID NO. 8503
STRAIN A909
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SEQUENCE LISTING

AGGTGAAA

SEQ ID NO. 8504
STRAIN H36B
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TG

SEQ ID NO. 8505
STRAIN 18RS21
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SEQ ID NO. 8506
STRAIN M732
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SEQ ID NO. 8507
STRAIN COH1
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SEQ ID NO. 8507
STRAIN M781
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SEQ ID NO. 8508
STRAIN CJB110
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SEQ ID NO. 8509
STRAIN 1169NT
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SEQ ID NO. 8510
STRAIN JM9130013

SEQUENCE LISTING

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SEQ ID NO. 8511
STRAIN 2603 frame: 1
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SEQ ID NO. 8512
STRAIN 090 frame: 1
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SEQ ID NO. 8513
STRAIN A909 frame: 1
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LIVPTSSVTNKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
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SEQ ID NO. 8514
STRAIN H36B frame: 1
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LIVPTSSVTNKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
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SEQUENCE LISTING

SEQ ID NO. 8515
STRAIN 18RS21 frame: 1
FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
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LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
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SEQ ID NO. 8516
STRAIN M732 frame: 1
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LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8517
STRAIN COH1 frame: 1
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LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
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SEQ ID NO. 8518
STRAIN M781 frame: 1
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EWEGKISYISNYPEAEANNNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
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SEQ ID NO. 8519
STRAIN M781 frame: 1
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LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
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SEQ ID NO. 8520
STRAIN CJB110 frame: 1
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LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
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SEQ ID NO. 8521
STRAIN 1169NT frame: 1
FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK

SEQUENCE LISTING

VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSSQ
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SEQ ID NO. 8522
STRAIN JM9130013 frame: 1
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SEQ ID NO. 8601
STRAIN 2603
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SEQ ID NO. 8602
STRAIN 090
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SEQ ID NO. 8603
STRAIN A909
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SEQUENCE LISTING

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SEQ ID NO. 8604
STRAIN H36B
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SEQ ID NO. 8605
STRAIN 18RS21
GAAGGCTTCACCTATTATGGA
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TAGAAAAAGATAGCCCCGTTTTTGGTAAACAACTGAAAGAAGCTAAAAAA
TTAACTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAAT
CATGGTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCAC
CAACTTTAGTTATTAAATATGGTGCACAAAATTATTTAgATaTGATGCCA
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CCAATGGAAAACTAAAACTCTCGCTGTCAAAAAAGATTTACACCATATCT
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GGTGGTTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
GCCCTTGTTAATATAAACAAAACgACTAAAAAAGCAGCTTCATCACTTAA
AGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCA
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GCTCAATTAAAATCATTTACAAA

SEQ ID NO. 8606
STRAIN M732
GAAGGCTTCACCTATTATGG
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CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAAA
GGGTGGTTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
TGCCCTTGTTAATATAAACAAAACGACTAAAAAAGCAGCTTCATCACTTA
AAGAAAGTGATGTCTGGAAGAAtTTACCAGCTGTCAAAAAAGGGCACATC
ATAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGA
AGCTCAATTAAAATCATTTACAAA

SEQ ID NO. 8607
STRAIN COH1
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AAGCTCAATTAAAATCATTTACAAA

SEQ ID NO. 8608
STRAIN M781
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SEQ ID NO. 8609
STRAIN CJB110
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TAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGAA
GCTCAATTAAAATCATTTACAAA

SEQ ID NO. 8610
STRAIN 1169NT
GAAGGCTTCACCTATTATGGAAAAATT
CCTGAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACACTGGGTA
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GTTAATATAAACAAAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAG
TGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAGAAA
GTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGAAGCTCAA
TTAAAATCATTTACAAA

SEQ ID NO. 8611
STRAIN JM9130013
GAAGGCTTCACCTATTATG
GAAAAATTCCTGAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTAC
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AAGCTCAATTAAAATCATTTACAAA

SEQ ID NO. 8612
STRAIN 2603 frame: 1
MKKIGIIVLTLLTFFLVSCGQQTKQESTKTTISKMPKIEGFTYYGKIPENPKKVINFTYS
YTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTADDTEAIAAQKPDLIMVFDQDPN
INTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEANQWVSQWKTKTLAVKKDLHHILK
PNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAPEKVKKDVFKKGWFTVSQEAIGD
YVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHIIESNYDVFYFSDPLSLEAQLKS
FTKAIKENTN

SEQ ID NO. 8613
STRAIN 090 frame: 1
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
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QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8614
STRAIN A909 frame: 1
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKGAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN

QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8615
STRAIN H36B frame: 1
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKGAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN
QWVSQWKTKTLAAKKDLHHILRPNTTFTIIDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8616
STRAIN 18RS21 frame: 1
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
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QWVSQWKTKTLAVKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8617
STRAIN M732 frame: 1
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8618
STRAIN COH1 frame: 1
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8619
STRAIN M781 frame: 1
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8620
STRAIN CJB110 frame: 1
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8621
STRAIN 1169NT frame: 1
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8622
STRAIN JM9130013 frame: 1
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKGAKKLTA
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SEQUENCE LISTING

QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
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IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8701
STRAIN 2603
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AAC

SEQ ID NO. 8702
STRAIN 090
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SEQUENCE LISTING

TAACTTACAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCT
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SEQ ID NO. 8703
STRAIN A909
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AAAACAACAA

SEQ ID NO. 8704
STRAIN 18RS21
GCAGAAGTGTCACAAGAACGCCCAGCGAAAAC
AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
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SEQUENCE LISTING

GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
GATTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAG
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ACAACAAACGTCCTTCA

SEQ ID NO. 8705
STRAIN M732
GCAGAAGTGTCACAAGAACGCCCAGCGAAAACAACAGT
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SEQ ID NO. 8706
STRAIN COH1
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SEQUENCE LISTING

TGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAG
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SEQ ID NO. 8707
STRAIN M781
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SEQ ID NO. 8708
STRAIN CJB110
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SEQ ID NO. 8709
STRAIN JM9130013
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ACGTCCTTCA

SEQ ID NO. 8710
STRAIN 2603 frame: 1
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KSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFKRYKVKTDISVDELKKLTTVEAAD
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PVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQDDAGYTIGEEFKWFLKSTIPANL
GDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHYTIDEPTVDNQNTLKITFKPEKFK
EIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVASTINEKAVLGKAIENTFELQYDHT
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AFAVKGMKRRTKDN

SEQ ID NO. 8711
STRAIN 090 frame: 1
AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
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SEQUENCE LISTING

TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
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ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8712
STRAIN 18RS21 frame: 1
AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVK.LGQ
DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8713
STRAIN M732 frame: 1
AEVSQERPAKTTVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
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VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
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ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8714
STRAIN M781 frame: 1
AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
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ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
R

SEQ ID NO. 8715
STRAIN COH1 frame: 1
AEVSQERPAKTAVNIYKLQADSYKSEITXNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
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VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8716
STRAIN CJB110 frame: 1
AEVSQERPAKTAVNIYKLQADSYKLEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
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VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
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ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNPKPTDITVDSADATPDTIKNNK
RPS

SEQUENCE LISTING

SEQ ID NO. 8717
STRAIN JM9130013 frame: 1
AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
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VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
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TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8718
STRAIN A909 frame: 1
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SEQ ID NO. 8801
STRAIN 2603
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SEQ ID NO. 8802
STRAIN H36B
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SEQ ID NO. 8803
STRAIN 18RS21
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SEQ ID NO. 8804
STRAIN M732
CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAG
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SEQ ID NO. 8805
STRAIN COH1
CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTT
GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTTAAAAAAACGCAA

SEQUENCE LISTING

AGAAGATGAAGAAGAACAAAAACGTATTAACGAAAAATTACGCTTAGATA
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SEQ ID NO. 8806
STRAIN M781
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SEQ ID NO. 8807
STRAIN CJB110
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SEQ ID NO. 8808
STRAIN 1169NT
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SEQ ID NO. 8809
STRAIN JM9130013
CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTT
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SEQ ID NO. 8810
STRAIN A909

SEQUENCE LISTING

CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTTGTC
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SEQ ID NO. 8811
STRAIN 090
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SEQ ID NO. 8812
STRAIN 2603 frame: 1
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FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8813
STRAIN H36B frame: 1
PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF

SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
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LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8814
STRAIN 18RS21 frame: 1
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NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
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QGQQIATEQAPNPQNVN

SEQ ID NO. 8815
STRAIN M732 frame: 1
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SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8816
STRAIN COH1 frame: 1
PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
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FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
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QGQQIATEQAPNPQNVN

SEQ ID NO. 8817
STRAIN M781 frame: 1
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FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8818
STRAIN CJB110 frame: 1
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FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8819
STRAIN 1169NT frame: 1
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FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
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SEQ ID NO. 8820
STRAIN JM9130013 frame: 1
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QGQQIATEQAPNPQNVN

SEQ ID NO. 8821
STRAIN A909 frame: 1
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FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIXIPLSKFKERLPFYKQIKKN
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QGQQIATEQAPNPQNVN

SEQ ID NO. 8822
STRAIN 090 frame: 2
KKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQN
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KDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKNL
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GQQIATEQAPNPQNVN

SEQ ID NO. 8901
STRAIN 2603
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CGTCGCTATATTGAAATT

SEQ ID NO. 8902

SEQUENCE LISTING

STRAIN 090
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SEQUENCE LISTING

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SEQUENCE LISTING

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AAATACATTATGATCAAGTGTTAGTAGTAGATGGTCATCAGTGGATTTCA
TACAAGAGTTATTCCGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8912
STRAIN 2603 frame: 1
MKKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNS
SNETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKE
TEVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRYAAIESLDPSGGS
ETKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILT
IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGF
DILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYN
IHLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQT
QFTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPN
LPKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRY
IEI

SEQ ID NO. 8913
STRAIN 090 frame: 1
KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
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EI

SEQUENCE LISTING

SEQ ID NO. 8914
STRAIN A909 frame: 1
KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
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EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8915
STRAIN H36B frame: 1
KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDDNNSS
NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
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EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8916
STRAIN 18RS21 frame: 1
KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8917
STRAIN M732 frame: 1
QVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSSNET
SASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKETEVK
NTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFGGVRRYAAIESLDPSGGSETKA
PTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTIEGN
QWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFDILI
TNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNIHLY
YQEASGTLVGVTGTKVTVAGTNSSQEPIENGLPKTGVYNIIGSTEVKNEAKISSQTQFTL
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GTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYIEI

SEQ ID NO. 8918
STRAIN COH1 frame: 1
KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFGGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLPKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQUENCE LISTING

SEQ ID NO. 8919
STRAIN M781 frame: 1
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NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFGGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLPKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8920
STRAIN CJB110 frame: 1
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NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8921
STRAIN 1169NT frame: 1
KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFGGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8922
STRAIN JM9130013 frame: 1
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NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTIYNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0001	453	chromosomal replication initiator protein DnaA
SAG0002	378	DNA polymerase III, beta subunit
SAG0003	293	diacylglycerol kinase catalytic domain protein, putative
SAG0004	65	conserved hypothetical protein
SAG0005	67	hypothetical protein
SAG0006	371	GTP-binding protein YchF
SAG0007	191	peptidyl-tRNA hydrolase
SAG0008	1165	transcription-repair coupling factor
SAG0009	31	hypothetical protein
SAG0010	90	S4 domain protein
SAG0011	123	cell division protein DivIC, putative
SAG0012	44	conserved hypothetical protein
SAG0013	428	protein of unknown function
SAG0014	424	MesJ/Ycf62 family protein
SAG0015	180	hypoxanthine-guanine phosphoribosyltransferase
SAG0016	658	cell division protein FtsH
SAG0017	447	pcsB protein
SAG0018	322	ribose-phosphate pyrophosphokinase
SAG0019	391	aminotransferase, class I
SAG0020	253	recombination protein O
SAG0021	283	protease, putative
SAG0022	330	fatty acid/phospholipid synthesis protein PlsX
SAG0023	79	acyl carrier protein
SAG0024	234	phosphoribosylaminoimidazole-succinocarboxamide synthase
SAG0025	1241	phosphoribosylformylglycinamidine synthase, putative
SAG0026	484	amidophosphoribosyltransferase
SAG0027	340	phosphoribosylformylglycinamidine cyclo-ligase
SAG0028	182	phosphoribosylglycinamide formyltransferase
SAG0029	250	acetyltransferase, GNAT family
SAG0030	515	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
SAG0031	299	peptidase, M23/M37 family
SAG0032	434	group B streptococcal surface immunogenic protein
SAG0033	232	N-acetylmannosamine-6-P epimerase, putative
SAG0034	438	sugar ABC transporter, sugar-binding protein
SAG0035	295	sugar ABC transporter, permease protein
SAG0036	276	sugar ABC transporter, permease protein
SAG0037	147	conserved hypothetical protein
SAG0038	220	conserved hypothetical protein
SAG0039	305	N-acetylneuraminate lyase, putative
SAG0040	293	ROK family protein
SAG0041	325	acetyl xylan esterase, putative
SAG0042	267	phosphosugar-binding transcriptional regulator, RpiR family, putative
SAG0043	421	phosphoribosylamine--glycine ligase
SAG0044	162	phosphoribosylaminoimidazole carboxylase, catalytic subunit
SAG0045	363	phosphoribosylaminoimidazole carboxylase, ATPase subunit
SAG0046	463	membrane protein, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0047	432	adenylosuccinate lyase
SAG0048	303	transcriptional regulator, Cro/CI family
SAG0049	332	Holliday junction DNA helicase RuvB
SAG0050	145	phosphotyrosine protein phosphatase, low molecular weight
SAG0051	126	MORN motif family protein
SAG0052	592	membrane protein, putative
SAG0053	880	aldehyde-alcohol dehydrogenase
SAG0054	338	alcohol dehydrogenase, propanol-preferring
SAG0055	496	threonine synthase
SAG0056	412	MATE efflux family protein
SAG0057	102	ribosomal protein S10
SAG0058	208	ribosomal protein L3
SAG0059	207	ribosomal protein L4
SAG0060	98	ribosomal protein L23
SAG0061	277	ribosomal protein L2
SAG0062	92	ribosomal protein S19
SAG0063	114	ribosomal protein L22
SAG0064	217	ribosomal protein S3
SAG0065	137	ribosomal protein L16
SAG0066	68	ribosomal protein L29
SAG0067	86	ribosomal protein S17
SAG0068	122	ribosomal protein L14
SAG0069	101	ribosomal protein L24
SAG0070	180	ribosomal protein L5
SAG0071	61	ribosomal protein S14, putative
SAG0072	132	ribosomal protein S8
SAG0073	178	ribosomal protein L6
SAG0074	118	ribosomal protein L18
SAG0075	164	ribosomal protein S5
SAG0076	59	ribosomal protein L30
SAG0077	146	ribosomal protein L15
SAG0078	434	preprotein translocase, SecY subunit
SAG0079	212	adenylate kinase
SAG0080	72	translation initiation factor IF-1
SAG0081	38	ribosomal protein L36
SAG0082	121	ribosomal protein S13
SAG0083	118	ribosomal protein S11
SAG0084	312	DNA-directed RNA polymerase, alpha subunit
SAG0085	128	ribosomal protein L17
SAG0086	85	lipoprotein, putative
SAG0087	59	hypothetical protein
SAG0088	56	hypothetical protein
SAG0089	183	conserved hypothetical protein
SAG0090	139	conserved hypothetical protein
SAG0091	144	transcriptional regulator ComX1, putative
SAG0092	230	phosphoglycerate mutase family protein
SAG0093	250	D-alanyl-D-alanine carboxypeptidase family protein
SAG0094	191	N-acetylmuramoyl-L-alanine amidase, family 4 protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0095	344	heat-inducible transcription repressor HrcA
SAG0096	190	heat shock protein GrpE
SAG0097	609	dnaK protein
SAG0098	379	dnaJ protein
SAG0099	415	transcriptional regulator, GntR family
SAG0100	258	tRNA pseudouridine synthase A
SAG0101	252	phosphomethylpyrimidine kinase, putative
SAG0102	154	conserved hypothetical protein
SAG0103	189	conserved hypothetical protein TIGR01440
SAG0104	280	conserved hypothetical protein
SAG0105	427	trigger factor
SAG0106	191	DNA-directed RNA polymerase, delta subunit, putative
SAG0107	534	CTP synthase
SAG0108	308	conserved hypothetical protein
SAG0109	148	deoxyuridine 5'-triphosphate nucleotidohydrolase
SAG0110	454	DNA repair protein RadA
SAG0111	165	carbonic anhydrase-related protein
SAG0112	439	pyridine nucleotide-disulphide oxidoreductase family protein
SAG0113	484	glutamyl-tRNA synthetase
SAG0114	322	ribose ABC transporter, periplasmic D-ribose-binding protein
SAG0115	310	ribose ABC transporter, permease protein
SAG0116	492	ribose ABC transporter, ATP-binding protein
SAG0117	132	ribose ABC transporter protein RbsD
SAG0118	303	ribokinase
SAG0119	328	ribose operon repressor RbsR
SAG0120	32	hypothetical protein
SAG0121	362	permease, putative
SAG0122	228	ABC transporter, ATP-binding protein
SAG0123	223	DNA-binding response regulator
SAG0124	356	sensor histidine kinase
SAG0125	396	argininosuccinate synthase
SAG0126	462	argininosuccinate lyase
SAG0127	293	fructose-bisphosphate aldolase
SAG0128	305	L-2-hydroxyisocaproate dehydrogenase
SAG0129	62	ribosomal protein L28
SAG0130	121	conserved hypothetical protein
SAG0131	543	DAK2 domain protein
SAG0132	294	SPFH domain/Band 7 family protein
SAG0133	38	conserved hypothetical protein
SAG0134	96	hypothetical protein
SAG0135	246	amino acid ABC transporter, ATP-binding protein
SAG0136	516	amino acid ABC transporter, amino acid-binding protein/permease protein
SAG0137	627	conserved hypothetical protein
SAG0138	279	undecaprenol kinase, putative
SAG0139	251	negative regulator of competence MecA, putative
SAG0140	386	glycosyl transferase, group 4 family protein
SAG0141	256	ABC transporter, ATP-binding protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0142	420	conserved hypothetical protein
SAG0143	410	selenocysteine lyase
SAG0144	147	NifU family protein
SAG0145	472	conserved hypothetical protein
SAG0146	395	penicillin-binding protein 4, putative
SAG0147	411	D-alanyl-D-alanine carboxypeptidase family protein
SAG0148	551	oligopeptide ABC transporter, substrate-binding protein, putative
SAG0149	304	oligopeptide ABC transporter, permease protein
SAG0150	343	oligopeptide ABC transporter, permease protein
SAG0151	348	oligopeptide ABC transporter, ATP-binding protein
SAG0152	310	oligopeptide ABC transporter, ATP-binding protein
SAG0153	283	4-diphosphocytidyl-2C-methyl-D-erythritol kinase
SAG0154	147	adc operon repressor AdcR
SAG0155	236	zinc ABC transporter, ATP-binding protein
SAG0156	270	zinc ABC transporter, permease protein
SAG0157	NA	deoxyribonuclease-related protein, degenerate
SAG0158	419	tyrosyl-tRNA synthetase
SAG0159	765	penicillin-binding protein 1B, putative
SAG0160	1191	DNA-directed RNA polymerase, beta subunit
SAG0161	1216	DNA-directed RNA polymerase beta' subunit
SAG0162	121	conserved hypothetical protein
SAG0163	323	competence protein CglA
SAG0164	282	competence protein CglB
SAG0165	151	conserved hypothetical protein
SAG0166	123	conserved domain protein
SAG0167	324	conserved hypothetical protein
SAG0168	397	acetate kinase
SAG0169	68	transcriptional regulator, Cro/CI family
SAG0170	45	hypothetical protein
SAG0171	151	hypothetical protein
SAG0172	221	protease, putative
SAG0173	256	pyrroline-5-carboxylate reductase
SAG0174	355	glutamyl-aminopeptidase
SAG0175	79	hypothetical protein
SAG0176	94	conserved hypothetical protein
SAG0177	107	thioredoxin family protein
SAG0178	208	tRNA binding domain protein
SAG0179	238	conserved hypothetical protein
SAG0180	131	single-strand binding protein
SAG0181	214	hydrolase, haloacid dehalogenase-like family
SAG0182	581	sensor histidine kinase, putative
SAG0183	246	response regulator
SAG0184	151	conserved hypothetical protein
SAG0185	242	membrane protein, putative
SAG0186	36	hypothetical protein
SAG0187	542	oligopeptide ABC transporter, oligopeptide-binding protein
SAG0188	325	oligopeptide ABC transporter, permease protein
SAG0189	273	oligopeptide ABC transporter, permease protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0190	267	peptide ABC transporter, ATP-binding protein
SAG0191	208	peptide ABC transporter, ATP-binding protein
SAG0192	676	PTS system, IIABC components
SAG0193	541	alpha amylase family protein
SAG0194	639	transcriptional antiterminator, BglG family
SAG0195	377	IS1548, transposase
SAG0196	66	conserved domain protein
SAG0197	94	PTS system, IIB component, putative
SAG0198	451	PTS system, IIC component, putative
SAG0199	285	transketolase, N-terminal subunit
SAG0200	309	transketolase, C-terminal subunit
SAG0201	419	oxidoreductase, putative
SAG0202	89	ribosomal protein S15
SAG0203	709	polyribonucleotide nucleotidyltransferase
SAG0204	250	conserved hypothetical protein
SAG0205	194	serine O-acetyltransferase
SAG0206	60	lipoprotein, putative
SAG0207	447	cysteinyl-tRNA synthetase
SAG0208	128	conserved hypothetical protein
SAG0209	251	RNA methyltransferase, TrmH family, group 3
SAG0210	172	conserved hypothetical protein
SAG0211	286	DegV family protein
SAG0212	32	hypothetical protein
SAG0213	39	hypothetical protein
SAG0214	148	ribosomal protein L13
SAG0215	130	ribosomal protein S9
SAG0216	33	hypothetical protein
SAG0217	384	site-specific recombinase, phage integrase family
SAG0218	158	transcriptional regulator, Cro/CI family
SAG0219	101	hypothetical protein
SAG0220	92	conserved hypothetical protein
SAG0221	76	hypothetical protein
SAG0222	108	conserved domain protein
SAG0223	209	conserved hypothetical protein, fusion
SAG0224	332	replication initiation protein, putative
SAG0225	144	hypothetical protein
SAG0226	418	recombination protein
SAG0227	156	hypothetical protein
SAG0228	111	conserved hypothetical protein
SAG0229	95	conserved hypothetical protein
SAG0230	96	conserved hypothetical protein
SAG0231	135	hypothetical protein
SAG0232	186	hypothetical protein
SAG0233	226	hypothetical protein
SAG0234	128	hypothetical protein
SAG0235	93	hypothetical protein
SAG0236	32	hypothetical protein
SAG0237	34	hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0238	41	hypothetical protein
SAG0239	286	transcriptional regulator MutR family
SAG0240	393	transporter, putative
SAG0241	213	amino acid ABC transporter, permease protein
SAG0242	308	amino acid ABC transporter, amino acid-binding protein
SAG0243	211	amino acid ABC transporter, permease protein
SAG0244	381	amino acid ABC transporter, ATP-binding protein
SAG0245	152	protein of unknown function/lipoprotein, putative
SAG0246	268	hypothetical protein
SAG0247	116	hypothetical protein
SAG0248	90	hypothetical protein
SAG0249	116	hypothetical protein
SAG0250	193	membrane protein, putative
SAG0251	72	transcriptional regulator, Cro/CI family
SAG0252	186	acetyltransferase, GNAT family
SAG0253	192	acetyltransferase, GNAT family
SAG0254	226	acetyltransferase, GNAT family
SAG0255	315	conserved hypothetical protein
SAG0256	163	RNA polymerase sigma factor, ECF subfamily
SAG0257	53	lipoprotein, putative
SAG0258	202	transcriptional regulator, TetR family
SAG0259	365	ABC transporter efflux protein, DrrB family, putative
SAG0260	238	ABC transporter, ATP-binding protein
SAG0261	129	IS1381, transposase OrfB
SAG0262	127	IS1381, transposase OrfA
SAG0263	171	hypothetical protein
SAG0264	103	conserved hypothetical protein
SAG0265	235	conserved hypothetical protein
SAG0266	382	N-acetylglucosamine-6-phosphate deacetylase
SAG0267	180	conserved hypothetical protein
SAG0268	304	glycyl-tRNA synthetase, alpha subunit
SAG0269	213	acyl carrier protein phosphodiesterase, putative
SAG0270	679	glycyl-tRNA synthetase, beta subunit
SAG0271	85	conserved hypothetical protein
SAG0272	87	membrane protein, putative
SAG0273	502	glycerol kinase
SAG0274	609	alpha-glycerophosphate oxidase
SAG0275	232	glycerol uptake facilitator protein
SAG0276	445	NADH oxidase, putative
SAG0277	476	conserved hypothetical protein
SAG0278	661	transketolase
SAG0279	101	conserved hypothetical protein
SAG0280	244	ABC transporter, ATP-binding protein
SAG0281	534	membrane protein, putative
SAG0282	461	PTS system, IIBC components
SAG0283	267	glutamate 5-kinase
SAG0284	417	gamma-glutamyl phosphate reductase
SAG0285	298	conserved hypothetical protein TIGR00006

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0286	108	cell division protein FtsL, putative
SAG0287	752	penicillin-binding protein 2X
SAG0288	336	phospho-N-acetylmuramoyl-pentapeptide-transferase
SAG0289	447	ATP-dependent RNA helicase, DEAD/DEAH box family
SAG0290	270	ABC transporter, substrate-binding protein
SAG0291	267	amino acid ABC transporter, permease protein
SAG0292	247	amino acid ABC transporter, ATP-binding protein
SAG0293	74	conserved hypothetical protein
SAG0294	304	thioredoxin reductase
SAG0295	486	conserved hypothetical protein
SAG0296	273	NAD synthetase
SAG0297	444	aminopeptidase C
SAG0298	750	penicillin-binding protein 1A
SAG0299	199	recombination protein U
SAG0300	172	conserved hypothetical protein
SAG0301	40	hypothetical protein
SAG0302	110	conserved hypothetical protein
SAG0303	384	conserved hypothetical protein
SAG0304	487	conserved hypothetical protein
SAG0305	160	autoinducer-2 production protein LuxS
SAG0306	535	KH domain protein
SAG0307	33	hypothetical protein
SAG0308	298	ABC transporter, ATP-binding protein
SAG0309	246	ABC transporter, permease protein, putative
SAG0310	361	conserved hypothetical protein
SAG0311	NA	DNA-binding response regulator, authentic point mutation
SAG0312	234	conserved hypothetical protein
SAG0313	209	guanylate kinase
SAG0314	104	DNA-directed RNA polymerase, omega subunit, putative
SAG0315	796	primosomal protein N'
SAG0316	311	methionyl-tRNA formyltransferase
SAG0317	440	sun protein
SAG0318	245	serine/threonine phosphatase, putative
SAG0319	651	serine/threonine protein kinase
SAG0320	231	conserved hypothetical protein
SAG0321	339	sensor histidine kinase, putative
SAG0322	213	DNA-binding response regulator
SAG0323	466	hydrolase, haloacid dehalogenase family/peptidyl-prolyl cis-trans isomerase, cyclophilin type
SAG0324	124	general stress protein, putative
SAG0325	258	pyruvate formate-lyase-activating enzyme
SAG0326	251	transcriptional regulator, DeoR family
SAG0327	327	transcriptional regulator, putative
SAG0328	107	PTS system, cellobiose-specific IIA component
SAG0329	106	PTS system, cellobiose-specific IIB component
SAG0330	433	PTS system, cellobiose-specific IIC component
SAG0331	818	formate acetyltransferase
SAG0332	222	transaldolase family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0333	362	glycerol dehydrogenase
SAG0334	308	cysteine synthase A
SAG0335	214	conserved hypothetical protein TIGR00257
SAG0336	429	helicase, putative
SAG0337	221	competence protein F, putative
SAG0338	184	ribosomal subunit interface protein
SAG0339	450	aspartate kinase family protein
SAG0340	216	hydrolase, haloacid dehalogenase-like family
SAG0341	49	hypothetical protein
SAG0342	263	enoyl-CoA hydratase/isomerase family protein
SAG0343	144	transcriptional regulator, MarR family
SAG0344	323	3-oxoacyl-(acyl-carrier-protein) synthase III
SAG0345	74	acyl carrier protein
SAG0346	319	enoyl-(acyl-carrier-protein) reductase II
SAG0347	308	malonyl CoA-acyl carrier protein transacylase
SAG0348	244	3-oxoacyl-[acyl-carrier protein] reductase
SAG0349	410	3-oxoacyl-(acyl-carrier-protein) synthase II
SAG0350	166	acetyl-CoA carboxylase, biotin carboxyl carrier protein
SAG0351	140	(3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase
SAG0352	456	acetyl-CoA carboxylase, biotin carboxylase
SAG0353	291	acetyl-CoA carboxylase, carboxyl transferase, beta subunit
SAG0354	257	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit
SAG0355	210	conserved hypothetical protein
SAG0356	425	seryl-tRNA synthetase
SAG0357	330	membrane protein, putative
SAG0358	120	conserved hypothetical protein
SAG0359	303	PTS system, mannose-specific IID component
SAG0360	270	PTS system, mannose-specific IIC component
SAG0361	336	PTS system, mannose-specific IIAB components
SAG0362	270	hydrolase, haloacid dehalogenase-like family
SAG0363	194	hypothetical protein
SAG0364	203	membrane protein, putative
SAG0365	473	xanthine/uracil permease family protein
SAG0366	169	conserved hypothetical protein TIGR00150
SAG0367	186	acetyltransferase, GNAT family
SAG0368	435	protein of unknown function
SAG0369	98	conserved hypothetical protein
SAG0370	139	HIT family protein
SAG0371	167	hypothetical protein
SAG0372	85	hypothetical protein
SAG0373	241	ABC transporter, ATP-binding protein
SAG0374	344	ABC transporter, permease protein
SAG0375	266	conserved hypothetical protein
SAG0376	211	conserved hypothetical protein TIGR00091
SAG0377	127	conserved hypothetical protein
SAG0378	379	N utilization substance protein A
SAG0379	98	conserved hypothetical protein
SAG0380	100	ribosomal protein L7A family

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0381	927	translation initiation factor IF-2
SAG0382	122	ribosome-binding factor A
SAG0383	334	protein of unknown function/lipoprotein, putative
SAG0384	138	transcriptional repressor CopY
SAG0385	744	copper-transporter ATPase CopA
SAG0386	68	copper-transporter protein CopZ
SAG0387	204	membrane protein, putative
SAG0388	270	hydrolase, haloacid dehalogenase-like family
SAG0389	880	DNA polymerase I
SAG0390	146	CoA-binding domain protein
SAG0391	159	transcriptional regulator, Fur family
SAG0392	521	cell wall surface anchor family protein
SAG0393	228	DNA-binding response regulator
SAG0394	345	sensor histidine kinase
SAG0395	246	membrane protein, putative
SAG0396	380	queuine tRNA-ribosyltransferase
SAG0397	102	conserved hypothetical protein
SAG0398	179	BioY family protein
SAG0399	258	AtsA/ElaC family protein
SAG0400	168	cytidine/deoxycytidylate deaminase family protein
SAG0401	44	hypothetical protein
SAG0402	449	glucose-6-phosphate isomerase
SAG0403	175	5-formyltetrahydrofolate cyclo-ligase family protein
SAG0404	225	rhomboid family protein
SAG0405	347	protein of unknown function/lipoprotein, putative
SAG0406	299	UTP-glucose-1-phosphate uridylyltransferase
SAG0407	338	glycerol-3-phosphate dehydrogenase (NAD(P)+)
SAG0408	109	ribonuclease P protein component
SAG0409	271	SpoIIIJ family protein
SAG0410	273	R3H domain protein
SAG0411	177	conserved hypothetical protein
SAG0412	258	recX protein
SAG0413	451	RNA methyltransferase, TrmA family
SAG0414	153	conserved hypothetical protein
SAG0415	142	acetyltransferase, GNAT family
SAG0416	1233	protease, putative
SAG0417	302	glycosyl transferase, group 2 family protein
SAG0418	336	ribonucleoside-diphosphate reductase 2, beta subunit
SAG0419	137	nrdI protein
SAG0420	721	ribonucleoside-diphosphate reductase 2, alpha subunit
SAG0421	1055	cell wall surface anchor family protein
SAG0422	129	conserved hypothetical protein
SAG0423	132	conserved domain protein
SAG0424	94	hypothetical protein
SAG0425	105	carboxymuconolactone decarboxylase family protein
SAG0426	131	conserved hypothetical protein
SAG0427	129	transcriptional regulator, MerR family
SAG0428	345	alcohol dehydrogenase, zinc-containing

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0429	284	oxidoreductase, aldo/keto reductase family
SAG0430	287	cation efflux system protein
SAG0431	174	transcriptional regulator, TetR family
SAG0432	397	transcriptional regulator, AraC family
SAG0433	1389	surface protein Rib
SAG0434	61	transposase, IS256 family, truncation
SAG0435	97	DNA-damage-inducible protein J, putative
SAG0436	62	hypothetical protein
SAG0437	123	lipoprotein, putative
SAG0438	145	bacteriophage L54a, integrase, truncation
SAG0439	NA	conserved hypothetical protein, degenerate
SAG0440	84	conserved hypothetical protein
SAG0441	103	conserved domain protein
SAG0442	189	acetyltransferase, GNAT family
SAG0443	194	acetyltransferase, GNAT family
SAG0444	188	conserved hypothetical protein
SAG0445	883	valyl-tRNA synthetase
SAG0446	319	oxidoreductase, Gfo/Idh/MocA family
SAG0447	287	magnesium transporter, CorA family
SAG0448	391	transposase, IS256 family
SAG0449	354	conserved hypothetical protein
SAG0450	330	aspartate--ammonia ligase
SAG0451	149	bacteriocin transport accessory protein, putative
SAG0452	179	type II DNA modification methyltransferase, putative
SAG0453	96	hypothetical protein
SAG0454	161	phosphopantetheine adenylyltransferase
SAG0455	357	conserved hypothetical protein
SAG0456	NA	conserved hypothetical protein, degenerate
SAG0457	192	conserved hypothetical protein
SAG0458	368	conserved hypothetical protein TIGR00048
SAG0459	171	VanZF domain protein
SAG0460	581	ABC transporter, ATP-binding/permease protein
SAG0461	579	ABC transporter, ATP-binding/permease protein
SAG0462	188	anthranilate synthase component II
SAG0463	179	BioY family protein
SAG0464	330	biotin synthetase
SAG0465	164	hypothetical protein
SAG0466	371	thiolase
SAG0467	409	AMP-binding enzyme domain protein
SAG0468	210	endonuclease III
SAG0469	131	type IV prepilin peptidase-related protein
SAG0470	69	conserved hypothetical protein
SAG0471	322	glucokinase
SAG0472	126	rhodanese-like family protein
SAG0473	613	elongation factor Tu family protein
SAG0474	81	conserved hypothetical protein
SAG0475	451	UDP-N-acetylmuramoylalanine--D-glutamate ligase
SAG0476	358	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
		pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
SAG0477	378	cell division protein DivIB, putative
SAG0478	429	cell division protein FtsA
SAG0479	426	cell division protein FtsZ
SAG0480	224	ylmE protein, putative
SAG0481	201	ylmF protein
SAG0482	84	YGGT family protein
SAG0483	262	ylmH protein
SAG0484	256	cell division protein DivIVA, putative
SAG0485	930	isoleucyl-tRNA synthetase
SAG0486	100	conserved hypothetical protein
SAG0487	151	MutT/nudix family protein
SAG0488	753	ATP-dependent Clp protease, ATP-binding subunit
SAG0489	34	hypothetical protein
SAG0490	76	conserved hypothetical protein
SAG0491	230	amino acid ABC transporter, permease protein
SAG0492	244	amino acid ABC transporter, ATP-binding protein
SAG0493	564	phosphoglucomutase/phosphomannomutase family protein
SAG0494	284	methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase
SAG0495	278	protein of unknown function
SAG0496	446	exodeoxyribonuclease VII, large subunit
SAG0497	71	exodeoxyribonuclease VII, small subunit
SAG0498	290	geranyltranstransferase, putative
SAG0499	275	hemolysin A
SAG0500	157	arginine repressor ArgR, putative
SAG0501	552	DNA repair protein RecN
SAG0502	278	DegV family protein
SAG0503	279	lipase/acylhydrolase
SAG0504	200	conserved hypothetical protein
SAG0505	91	DNA-binding protein HU
SAG0506	65	hypothetical protein
SAG0507	310	dihydroorotate dehydrogenase A
SAG0508	411	beta-lactam resistance factor
SAG0509	403	beta-lactam resistance factor
SAG0510	406	murM protein, putative
SAG0511	270	hydrolase, haloacid dehalogenase-like family
SAG0512	438	HD domain protein
SAG0513	128	conserved hypothetical protein
SAG0514	894	cation-transporting ATPase, E1-E2 family
SAG0515	286	conserved hypothetical protein
SAG0516	643	fructose-1,6-bisphosphatase, putative
SAG0517	374	iron-sulfur cluster-binding protein, putative
SAG0518	NA	peptide chain release factor 2, programmed frameshift
SAG0519	230	cell division ABC transporter, ATP-binding protein FtsE
SAG0520	309	cell division ABC transporter, permease protein FtsX
SAG0521	236	carboxymethylenebutenolidase-related protein
SAG0522	232	metallo-beta-lactamase superfamily protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0523	254	oxidoreductase, short chain dehydrogenase/reductase family
SAG0524	835	DNA polymerase III, epsilon subunit/ATP-dependent helicase DinG
SAG0525	397	aspartate aminotransferase
SAG0526	448	asparaginyl-tRNA synthetase
SAG0527	185	conserved hypothetical protein
SAG0528	327	inosine-uridine preferring nucleoside hydrolase
SAG0529	38	hypothetical protein
SAG0530	137	OsmC/Ohr family protein
SAG0531	296	conserved hypothetical protein
SAG0532	324	conserved hypothetical protein
SAG0533	303	conserved hypothetical protein
SAG0534	465	dipeptidase
SAG0535	506	zinc ABC transporter, zinc-binding adhesion liprotein
SAG0536	86	ribosomal protein L31
SAG0537	311	DHH family protein
SAG0538	340	adenosine deaminase, putative
SAG0539	147	flavodoxin
SAG0540	91	chorismate mutase, putative
SAG0541	398	voltage-gated chloride channel family protein
SAG0542	127	IS1381, transposase OrfA
SAG0543	129	IS1381, transposase OrfB
SAG0544	115	ribosomal protein L19
SAG0545	359	prophage LambdaSa1, site-specific recombinase, phage integrase family
SAG0546	67	conserved domain protein
SAG0547	185	hypothetical protein
SAG0548	265	prophage LambdaSa1, repressor protein, putative
SAG0549	47	hypothetical protein
SAG0550	74	conserved hypothetical protein
SAG0551	52	conserved hypothetical protein
SAG0552	62	hypothetical protein
SAG0553	268	hypothetical protein
SAG0554	63	prophage LambdaSa1, transcriptional regulator, Cro/CI family
SAG0555	249	prophage LambdaSa1, antirepressor, putative
SAG0556	47	hypothetical protein
SAG0557	76	hypothetical protein
SAG0558	74	hypothetical protein
SAG0559	286	conserved hypothetical protein
SAG0560	77	conserved hypothetical protein
SAG0561	46	hypothetical protein
SAG0562	84	hypothetical protein
SAG0563	53	hypothetical protein
SAG0564	160	conserved hypothetical protein
SAG0565	224	conserved domain protein
SAG0566	138	prophage LambdaSa1, single-strand binding protein
SAG0567	439	prophage LambdaSa1, reverse transcriptase/maturase family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0568	67	conserved hypothetical protein
SAG0569	158	conserved hypothetical protein
SAG0570	115	hypothetical protein
SAG0571	43	hypothetical protein
SAG0572	138	conserved hypothetical protein
SAG0573	54	hypothetical protein
SAG0574	89	conserved hypothetical protein
SAG0575	110	hypothetical protein
SAG0576	43	hypothetical protein
SAG0577	177	conserved hypothetical protein
SAG0578	88	conserved hypothetical protein
SAG0579	142	conserved hypothetical protein
SAG0580	111	conserved hypothetical protein, truncation
SAG0581	118	conserved hypothetical protein
SAG0582	422	conserved hypothetical protein
SAG0583	406	conserved hypothetical protein
SAG0584	62	conserved hypothetical protein, truncation
SAG0585	471	conserved hypothetical protein
SAG0586	154	conserved hypothetical protein
SAG0587	300	prophage LambdaSa1, structural protein, putative
SAG0588	71	conserved hypothetical protein
SAG0589	143	conserved hypothetical protein
SAG0590	112	conserved hypothetical protein
SAG0591	78	conserved hypothetical protein
SAG0592	111	conserved hypothetical protein
SAG0593	185	prophage LambdaSa1, structural protein
SAG0594	81	conserved hypothetical protein
SAG0595	123	conserved hypothetical protein
SAG0596	670	prophage LambdaSa1, pblA protein, internal deletion
SAG0597	506	prophage LambdaSa1, minor structural protein, putative
SAG0598	1374	prophage LambdaSa1, N-acetylmuramoyl-L-alanine amidase, family 4
SAG0599	668	prophage LambdaSa1, minor structural protein, putative
SAG0600	109	hypothetical protein
SAG0601	70	hypothetical protein
SAG0602	100	conserved hypothetical protein
SAG0603	111	conserved hypothetical protein
SAG0604	239	prophage LambdaSa1, lysin, putative
SAG0605	323	conserved hypothetical protein
SAG0606	66	conserved hypothetical protein
SAG0607	56	conserved hypothetical protein
SAG0608	59	hypothetical protein
SAG0609	NA	prophage LambdaSa1, integrase, degenerate
SAG0610	134	conserved hypothetical protein
SAG0611	NA	transposase, degenerate
SAG0612	53	conserved hypothetical protein
SAG0613	425	transmembrane protein Vexp1
SAG0614	218	ABC transporter, ATP-binding protein Vexp2

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0615	458	transmembrane protein Vexp3
SAG0616	217	DNA-binding response regulator VncR
SAG0617	439	sensor histidine kinase VncS
SAG0618	195	transposase OrfB, IS3 family, truncation
SAG0619	66	conserved hypothetical protein
SAG0620	62	hypothetical protein
SAG0621	401	rod shape-determining protein RodA, putative☐
SAG0622	186	hydrolase, haloacid dehalogenase-like family
SAG0623	650	DNA gyrase, B subunit
SAG0624	574	septation ring formation regulator EzrA, putative
SAG0625	213	phosphoserine phosphatase SerB
SAG0626	161	MutT/nudix family protein
SAG0627	151	conserved hypothetical protein
SAG0628	435	enolase
SAG0629	354	conserved domain protein
SAG0630	427	3-phosphoshikimate 1-carboxyvinyltransferase
SAG0631	170	shikimate kinase
SAG0632	457	psr protein
SAG0633	451	RNA methyltransferase, TrmA family
SAG0634	70	hypothetical protein
SAG0635	245	acid phosphatase, class B
SAG0636	172	conserved hypothetical protein
SAG0637	NA	transcriptional regulator, TetR family, putative, authentic frameshift
SAG0638	109	cell wall surface anchor family protein, truncation
SAG0639	273	transposase OrfB, IS3 family
SAG0640	91	transposase OrfA, IS3 family
SAG0641	NA	Tn5252, Orf 10 protein, degenerate
SAG0642	59	hypothetical protein
SAG0643	NA	chaperonin, 33 kDa, degenerate
SAG0644	402	transcriptional regulator, AraC family
SAG0645	554	cell wall surface anchor family protein
SAG0646	307	cell wall surface anchor family protein
SAG0647	305	sortase family protein
SAG0648	260	sortase family protein
SAG0649	890	cell wall surface anchor family protein, putative
SAG0650	189	sortase family protein
SAG0651	201	protein of unknown function
SAG0652	NA	Tn5252, Orf 28 protein, degenerate
SAG0653	NA	conserved hypothetical protein, degenerate
SAG0654	34	hypothetical protein
SAG0655	57	conserved hypothetical protein
SAG0656	36	hypothetical protein
SAG0657	89	hypothetical protein
SAG0658	383	lipoprotein, putative
SAG0659	330	ABC transporter, ATP-binding protein
SAG0660	272	membrane protein
SAG0661	261	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0662	101	cylX protein
SAG0663	282	cylD protein
SAG0664	240	cylG protein
SAG0665	101	acyl carrier protein AcpC
SAG0666	158	cylZ protein
SAG0667	309	cylA protein
SAG0668	292	cylB protein
SAG0669	667	cylE protein
SAG0670	317	cylF protein
SAG0671	731	cylI protein
SAG0672	403	cylJ protein
SAG0673	191	cylK protein
SAG0674	113	hypothetical protein
SAG0675	171	putative secreted protein
SAG0676	885	proteinase, putative
SAG0677	1062	hypothetical protein
SAG0678	NA	endopeptidase O, degenerate
SAG0679	343	protein of unknown function
SAG0680	339	protein of unknown function
SAG0681	353	conserved domain protein
SAG0682	409	permease, putative
SAG0683	NA	transmembrane protein Vexp3, putative, degenerate
SAG0684	223	ABC transporter, ATP-binding protein
SAG0685	472	conserved hypothetical protein
SAG0686	261	DNA-entry nuclease, putative
SAG0687	212	DedA family protein, putative
SAG0688	218	ABC transporter, ATP-binding protein
SAG0689	257	membrane protein, putative
SAG0690	272	conserved hypothetical protein
SAG0691	294	transcriptional regulator, LysR family
SAG0692	193	regulatory protein, putative
SAG0693	377	IS1548, transposase
SAG0694	173	regulatory protein, putative, truncation
SAG0695	330	D-lactate dehydrogenase
SAG0696	516	sodium:galactoside symporter family protein, putative
SAG0697	341	2-keto-3-deoxygluconate kinase
SAG0698	599	beta-glucuronidase
SAG0699	223	transcriptional regulator, GntR family
SAG0700	205	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase
SAG0701	466	glucuronate isomerase
SAG0702	348	mannonate dehydratase
SAG0703	279	D-mannonate oxidoreductase
SAG0704	270	hydrolase, haloacid dehalogenase-like family
SAG0705	596	glycosyl hydrolase, family 3
SAG0706	361	proline dipeptidase
SAG0707	334	transcriptional regulator, RegM family
SAG0708	488	alpha amylase family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0709	332	glycosyl transferase, group 1 family protein
SAG0710	444	glycosyl transferase, group 1 family protein
SAG0711	647	threonyl-tRNA synthetase
SAG0712	234	DNA-binding response regulator
SAG0713	339	conserved hypothetical protein
SAG0714	188	conserved hypothetical protein
SAG0715	216	amino acid ABC transporter, permease protein
SAG0716	231	amino acid ABC transporter, permease protein
SAG0717	266	amino acid ABC transporter, amino acid-binding protein
SAG0718	251	amino acid ABC transporter, ATP-binding protein
SAG0719	236	DNA-binding response regulator
SAG0720	449	sensory box histidine kinase
SAG0721	269	metallo-beta-lactamase superfamily protein
SAG0722	122	conserved hypothetical protein
SAG0723	236	ribonuclease III
SAG0724	1179	chromosome segregation SMC protein
SAG0725	265	hydrolase, haloacid dehalogenase-like family
SAG0726	274	hydrolase, haloacid dehalogenase-like family
SAG0727	536	signal recognition particle-docking protein FtsY
SAG0728	270	ABC transporter, substrate-binding protein
SAG0729	300	ABC transporter, permease protein, putative
SAG0730	42	ABC transporter, ATP-binding protein
SAG0731	347	bacterial luciferase family protein
SAG0732	720	transcriptional accessory protein Tex, putative
SAG0733	142	conserved hypothetical protein
SAG0734	87	phage shock protein C, putative
SAG0735	44	hypothetical protein
SAG0736	311	HPr(Ser) kinase/phosphatase
SAG0737	257	prolipoprotein diacylglyceryl transferase
SAG0738	132	conserved hypothetical protein
SAG0739	143	conserved hypothetical protein
SAG0740	91	conserved hypothetical protein
SAG0741	303	peptidase, U32 family, putative
SAG0742	428	peptidase, U32 family
SAG0743	70	conserved hypothetical protein
SAG0744	265	membrane protein, putative
SAG0745	446	Mn2+/Fe2+ transporter, NRAMP family
SAG0746	369	riboflavin biosynthesis protein RibD
SAG0747	208	riboflavin synthase, alpha subunit
SAG0748	397	riboflavin biosynthesis protein RibA
SAG0749	156	riboflavin synthase, beta subunit
SAG0750	496	lysyl-tRNA synthetase
SAG0751	300	hydrolase, haloacid dehalogenase-like family
SAG0752	213	phosphoglycerate mutase family protein
SAG0753	157	ebsC family protein, putative
SAG0754	205	conserved domain protein
SAG0755	282	peptidase, U32 family
SAG0756	174	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0757	129	protein of unknown function/lipoprotein, putative
SAG0758	599	oligoendopeptidase F, putative
SAG0759	931	phosphoenolpyruvate carboxylase
SAG0760	377	IS1548, transposase
SAG0761	422	cell division protein, FtsW/RodA/SpoVE family
SAG0762	398	translation elongation factor Tu
SAG0763	252	triosephosphate isomerase
SAG0764	230	phosphoglycerate mutase family protein
SAG0765	681	penicillin-binding protein 2b
SAG0766	198	recombination protein RecR
SAG0767	348	D-alanine--D-alanine ligase
SAG0768	455	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase
SAG0769	406	oxalate:formate antiporter
SAG0770	228	membrane protein, putative
SAG0771	512	cell wall surface anchor family protein
SAG0772	514	peptide chain release factor 3
SAG0773	126	conserved hypothetical protein
SAG0774	244	ABC transporter, ATP-binding protein
SAG0775	220	ABC transporter, permease protein
SAG0776	276	YaeC family protein, putative
SAG0777	528	ATP-dependent RNA helicase, DEAD/DEAH box family
SAG0778	88	conserved hypothetical protein
SAG0779	254	conserved hypothetical protein
SAG0780	246	acyltransferase family protein
SAG0781	217	competence protein CelA
SAG0782	745	DNA internalization-related competence protein ComEC/Rec2
SAG0783	269	hydrolase, haloacid dehalogenase-like family
SAG0784	314	sugar-binding transcriptional regulator, LacI family
SAG0785	330	conserved hypothetical protein
SAG0786	242	conserved domain protein
SAG0787	345	DNA polymerase III, delta subunit, putative
SAG0788	202	superoxide dismutase, Fe-Mn
SAG0789	283	transcriptional antiterminator LicT
SAG0790	622	PTS system, beta-glucosides-specific IIABC components
SAG0791	475	6-phospho-beta-glucosidase
SAG0792	364	conserved hypothetical protein
SAG0793	380	glycerate kinase 2
SAG0794	418	permease, GntP family
SAG0795	354	conserved hypothetical protein
SAG0796	147	transcriptional regulator, MarR family
SAG0797	342	S-adenosylmethionine:tRNA ribosyltransferase-isomerase
SAG0798	226	membrane protein, putative
SAG0799	233	glucosamine-6-phosphate isomerase
SAG0800	318	glutathione S-transferase family protein
SAG0801	239	ribosomal small subunit pseudouridine synthase A
SAG0802	38	hypothetical protein
SAG0803	383	major facilitator family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0804	315	competence protein CoiA
SAG0805	601	oligoendopeptidase B
SAG0806	208	hydrolase, haloacid dehalogenase-like family
SAG0807	235	O-methyltransferase family protein
SAG0808	309	protease maturation protein, putative
SAG0809	161	conserved hypothetical protein
SAG0810	872	alanyl-tRNA synthetase
SAG0811	238	membrane protein, putative
SAG0812	272	glycosyl transferase, family 8
SAG0813	81	hypothetical protein
SAG0814	95	conserved hypothetical protein
SAG0815	71	transcriptional regulator, Cro/CI family
SAG0816	253	membrane protein, putative
SAG0817	187	membrane protein, putative
SAG0818	319	ribonucleoside-diphosphate reductase 2, beta subunit
SAG0819	719	ribonucleoside-diphosphate reductase 2, alpha subunit
SAG0820	74	ribonucleoside-diphosphate reductase 2, NrdH-redoxin
SAG0821	87	phosphocarrier protein HPr
SAG0822	577	phosphoenolpyruvate-protein phosphotransferase
SAG0823	475	glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent
SAG0824	417	polysaccharide deacetylase family protein
SAG0825	360	ATP-dependent RNA helicase, DEAD/DEAH box family
SAG0826	209	uridine kinase
SAG0827	165	conserved hypothetical protein
SAG0828	554	DNA polymerase III, gamma and tau subunits
SAG0829	64	conserved hypothetical protein
SAG0830	311	biotin--acetyl-CoA-carboxylase ligase
SAG0831	398	S-adenosylmethionine synthetase
SAG0832	753	protein of unknown function
SAG0833	181	hypothetical protein
SAG0834	42	hypothetical protein
SAG0835	188	conserved hypothetical protein
SAG0836	184	conserved hypothetical protein
SAG0837	428	ABC transporter, ATP-binding protein
SAG0838	233	hypothetical protein
SAG0839	226	transcriptional regulator, TenA family
SAG0840	265	phosphomethylpyrimidine kinase
SAG0841	256	hydroxyethylthiazole kinase
SAG0842	223	thiamine-phosphate pyrophosphorylase
SAG0843	419	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
SAG0844	184	acetyltransferase, GNAT family
SAG0845	427	CBS domain protein
SAG0846	286	methionine aminopeptidase, type I
SAG0847	306	ribonuclease BN, putative
SAG0848	151	GtrA family protein
SAG0849	169	conserved hypothetical protein
SAG0850	652	DNA ligase, NAD-dependent
SAG0851	339	bmrU protein, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0852	766	pullulanase, putative
SAG0853	622	1,4-alpha-glucan branching enzyme
SAG0854	379	glucose-1-phosphate adenylyltransferase
SAG0855	NA	glycogen biosynthesis protein GlgD, authentic frameshift
SAG0856	476	glycogen synthase
SAG0857	66	ATP synthase F0, C subunit
SAG0858	238	ATP synthase F0, A subunit
SAG0859	165	ATP synthase F0, B subunit
SAG0860	178	ATP synthase F1, delta subunit
SAG0861	501	ATP synthase F1, alpha subunit
SAG0862	293	ATP synthase F1, gamma subunit
SAG0863	468	ATP synthase F1, beta subunit
SAG0864	137	ATP synthase F1, epsilon subunit
SAG0865	76	conserved hypothetical protein
SAG0866	423	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
SAG0867	63	conserved hypothetical protein
SAG0868	285	DNA-entry nuclease
SAG0869	346	phenylalanyl-tRNA synthetase, alpha subunit
SAG0870	173	acetyltransferase, GNAT family
SAG0871	801	phenylalanyl-tRNA synthetase, beta subunit
SAG0872	300	conserved hypothetical protein
SAG0873	1077	exonuclease RexB
SAG0874	1207	exonuclease RexA
SAG0875	305	magnesium transporter, CorA family, putative
SAG0876	458	tRNA modification GTPase TrmE
SAG0877	636	ABC transporter, ATP-binding protein
SAG0878	322	acetoin dehydrogenase, thymine PPi dependent, E1 component, alpha subunit
SAG0879	332	acetoin dehydrogenase, thymine PPi dependent, E1 component, beta subunit
SAG0880	462	acetoin dehydrogenase, thymine PPi dependent, E2 component, dihydrolipoamide acetyltransferase
SAG0881	585	acetoin dehydrogenase, thymine PPi dependent, E3 component, dihydrolipoamide dehydrogenase
SAG0882	329	lipoate-protein ligase A
SAG0883	261	cobyric acid synthase, putative
SAG0884	447	mur ligase family protein
SAG0885	283	conserved hypothetical protein TIGR00159
SAG0886	319	protein of unknown function
SAG0887	450	phosphoglucomutase/phosphomannomutase family protein
SAG0888	123	conserved hypothetical protein
SAG0889	126	conserved hypothetical protein
SAG0890	376	oxygen-independent coproporphyrinogen III oxidase, putative
SAG0891	245	conserved hypothetical protein
SAG0892	256	hydrolase, haloacid dehalogenase-like family
SAG0893	218	conserved hypothetical protein
SAG0894	1370	protein of unknown function
SAG0895	289	lipoyl-binding domain protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0896	108	oxidoreductase, putative
SAG0897	221	conserved hypothetical protein
SAG0898	83	hypothetical protein
SAG0899	57	hypothetical protein
SAG0900	56	hypothetical protein
SAG0901	127	hypothetical protein
SAG0902	45	hypothetical protein
SAG0903	44	hypothetical protein
SAG0904	56	hypothetical protein
SAG0905	138	nucleoside diphosphate kinase
SAG0906	610	GTP-binding protein LepA
SAG0907	877	protein of unknown function/lipoprotein, putative
SAG0908	203	HD domain protein
SAG0909	154	acetyltransferase, GNAT family
SAG0910	144	PilB-related protein
SAG0911	930	cation-transporting ATPase, E1-E2 family
SAG0912	367	nucleoside diphosphate kinase domain protein
SAG0913	212	chloramphenicol acetyltransferase
SAG0914	203	conserved hypothetical protein
SAG0915	405	Tn916, transposase
SAG0916	67	Tn916, excisionase
SAG0917	83	Tn916, hypothetical protein
SAG0918	76	Tn916, hypothetical protein
SAG0919	157	Tn916, hypothetical protein
SAG0920	23	Tn916, hypothetical protein
SAG0921	117	Tn916, transcriptional regulator, putative
SAG0922	61	Tn916, hypothetical protein
SAG0923	639	Tn916, tetracycline resistance protein
SAG0924	28	Tn916, tetM leader peptide
SAG0925	310	Tn916, hypothetical protein
SAG0926	333	Tn916, NLP/P60 family protein
SAG0927	725	membrane protein, putative
SAG0928	NA	Tn916, hypothetical protein, authentic frameshift
SAG0929	168	Tn916, hypothetical protein
SAG0930	165	Tn916, hypothetical protein
SAG0931	73	Tn916, hypothetical protein
SAG0932	401	Tn916, transcriptional regulator, putative
SAG0933	461	Tn916, FtsK/SpoIIIE family protein
SAG0934	128	Tn916, hypothetical protein
SAG0935	104	Tn916, hypothetical protein
SAG0936	39	Tn916, hypothetical protein
SAG0937	NA	ABC transporter, ATP-binding protein, authentic frameshift
SAG0938	122	transcriptional regulator, GntR family
SAG0939	1034	DNA polymerase III, alpha subunit
SAG0940	340	6-phosphofructokinase
SAG0941	500	pyruvate kinase
SAG0942	185	signal peptidase I, putative
SAG0943	47	hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0944	604	glucosamine--fructose-6-phosphate aminotransferase, isomerizing
SAG0945	377	IS1548, transposase
SAG0946	109	phnA protein
SAG0947	213	amino acid ABC transporter, permease protein
SAG0948	209	amino acid ABC transporter, ATP-binding protein
SAG0949	276	amino acid ABC transporter, amino acid-binding protein
SAG0950	82	ribosomal protein S20
SAG0951	306	pantothenate kinase
SAG0952	196	conserved hypothetical protein
SAG0953	129	cytidine deaminase
SAG0954	349	protein of unknown function/lipoprotein, putative
SAG0955	511	sugar ABC transporter, ATP-binding protein
SAG0956	353	sugar ABC transporter, permease protein, putative
SAG0957	318	sugar ABC transporter, permease protein, putative
SAG0958	456	NADH oxidase
SAG0959	329	L-lactate dehydrogenase
SAG0960	819	DNA gyrase, A subunit
SAG0961	247	sortase SrtA
SAG0962	137	glyoxylase family protein
SAG0963	320	conserved hypothetical protein
SAG0964	375	Na+/H+ exchanger family protein
SAG0965	127	IS1381, transposase OrfA
SAG0966	129	IS1381, transposase OrfB
SAG0967	520	GMP synthase
SAG0968	232	transcriptional regulator, GntR family
SAG0969	444	gid protein
SAG0970	247	acetyltransferase, GNAT family
SAG0971	282	protein of unknown function/lipoprotein, putative
SAG0972	NA	conserved hypothetical protein, authentic frameshift
SAG0973	320	nisin-resistance protein, putative
SAG0974	250	ABC transporter, ATP-binding protein
SAG0975	651	ABC transporter, permease protein, putative
SAG0976	222	DNA-binding response regulator
SAG0977	312	sensor histidine kinase
SAG0978	356	site-specific recombinase, phage integrase family
SAG0979	553	ABC transporter, substrate-binding protein
SAG0980	257	conserved hypothetical protein
SAG0981	228	satD protein
SAG0982	521	signal recognition particle protein Ffh
SAG0983	110	conserved hypothetical protein
SAG0984	437	sensor histidine kinase CiaH
SAG0985	226	DNA-binding response regulator CiaR
SAG0986	849	aminopeptidase N
SAG0987	217	phosphate transport system regulatory protein PhoU
SAG0988	252	phosphate ABC transporter, ATP-binding protein PstB, putative
SAG0989	267	phosphate ABC transporter, ATP-binding protein PstB, putative
SAG0990	295	phosphate ABC transporter, permease protein PstA, putative
SAG0991	305	phosphate ABC transporter, permease protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0992	286	phosphate ABC transporter, phosphate-binding protein
SAG0993	436	NOL1/NOP2/sun family protein
SAG0994	254	inositol monophosphatase family protein
SAG0995	93	conserved hypothetical protein
SAG0996	137	conserved hypothetical protein
SAG0997	310	macrolide-efflux protein mreA/riboflavin biosynthesis protein RibF
SAG0998	294	tRNA pseudouridine synthase B
SAG0999	143	acetyltransferase, GNAT family
SAG1000	423	conserved hypothetical protein
SAG1001	196	conserved hypothetical protein
SAG1002	292	protease, putative
SAG1003	876	permease, putative
SAG1004	233	ABC transporter, ATP-binding protein
SAG1005	706	DNA topoisomerase I
SAG1006	280	DprA/SMF protein, putative DNA processing factor
SAG1007	342	iron-compound ABC transporter, iron-compound-binding protein
SAG1008	253	iron compound ABC transporter, ATP-binding protein
SAG1009	324	iron compound ABC transporter, permease protein
SAG1010	320	iron compound ABC transporter, permease protein
SAG1011	182	acetyltransferase, CysE/LacA/LpxA/NodL family
SAG1012	253	ribonuclease HII
SAG1013	283	GTP-binding protein
SAG1014	190	conserved hypothetical protein
SAG1015	494	carbon starvation protein CstA, putative
SAG1016	244	response regulator
SAG1017	579	sensor histidine kinase, putative
SAG1018	40	lipoprotein, putative
SAG1019	39	hypothetical protein
SAG1020	227	lipoprotein, putative
SAG1021	107	hypothetical protein
SAG1022	177	hypothetical protein
SAG1023	48	hypothetical protein
SAG1024	183	lipoprotein, putative
SAG1025	149	hypothetical protein
SAG1026	NA	immunogenic secreted protein, degenerate
SAG1027	84	conserved hypothetical protein
SAG1028	196	hypothetical protein
SAG1029	101	hypothetical protein
SAG1030	304	protein of unknown function
SAG1031	120	conserved domain protein
SAG1032	85	conserved hypothetical protein
SAG1033	1309	FtsK/SpoIIIE family protein
SAG1034	55	hypothetical protein
SAG1035	424	conserved hypothetical protein
SAG1036	80	conserved hypothetical protein
SAG1037	157	hypothetical protein
SAG1038	1003	phage infection protein, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1039	96	conserved hypothetical protein
SAG1040	260	conserved domain protein
SAG1041	107	hypothetical protein
SAG1042	1060	carbamoyl-phosphate synthase, large subunit
SAG1043	358	carbamoyl-phosphate synthase, small subunit
SAG1044	307	aspartate carbamoyltransferase
SAG1045	430	dihydroorotase, multifunctional complex type
SAG1046	209	orotate phosphoribosyltransferase
SAG1047	233	orotidine 5'-phosphate decarboxylase
SAG1048	410	membrane protein, putative
SAG1049	513	ABC transporter, ATP-binding protein
SAG1050	112	ribonucleotide reductase, truncation
SAG1051	358	aspartate-semialdehyde dehydrogenase
SAG1052	47	cell wall surface anchor family protein, putative
SAG1053	30	hypothetical protein
SAG1054	531	cardiolipin synthetase
SAG1055	556	formate--tetrahydrofolate ligase
SAG1056	339	lipoate-protein ligase A
SAG1057	292	conserved hypothetical protein
SAG1058	272	conserved hypothetical protein
SAG1059	110	glycine cleavage system H protein, putative
SAG1060	328	bacterial luciferase family protein
SAG1061	399	oxidoreductase, FMN-binding
SAG1062	282	lipoate-protein ligase A family protein
SAG1063	228	flavoprotein-related protein
SAG1064	180	flavoprotein family protein
SAG1065	190	membrane protein, putative
SAG1066	572	phosphoglucomutase
SAG1067	178	IS861, transposase OrfA
SAG1068	277	IS861, transposase OrfB
SAG1069	65	hypothetical protein
SAG1070	577	ABC transporter, ATP-binding/permease protein
SAG1071	573	ABC transporter, ATP-binding/permease protein
SAG1072	200	conserved hypothetical protein
SAG1073	325	conserved hypothetical protein
SAG1074	418	serine hydroxymethyltransferase
SAG1075	183	Sua5/YciO/YrdC/YwlC family protein
SAG1076	276	modification methylase, HemK family
SAG1077	359	peptide chain release factor 1
SAG1078	189	thymidine kinases
SAG1079	60	4-oxalocrotonate tautomerase
SAG1080	47	hypothetical protein
SAG1081	312	ApbE family protein
SAG1082	200	conserved hypothetical protein
SAG1083	411	conserved hypothetical protein
SAG1084	262	formate/nitrite transporter family protein
SAG1085	424	xanthine permease
SAG1086	193	xanthine phosphoribosyltransferase

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1087	327	guanosine monophosphate reductase
SAG1088	446	drug resistance transporter, EmrB/QacA family, putative
SAG1089	230	conserved hypothetical protein
SAG1090	666	potassium uptake protein, putative
SAG1091	216	oxidoreductase, short chain dehydrogenase/reductase family
SAG1092	330	phosphate acetyltransferase
SAG1093	294	ribosomal large subunit pseudouridine synthase, RluD subfamily
SAG1094	278	conserved hypothetical protein
SAG1095	223	GTP pyrophosphokinase family protein
SAG1096	190	conserved hypothetical protein
SAG1097	324	ribose-phosphate pyrophosphokinase
SAG1098	371	cysteine desulphurase
SAG1099	115	conserved hypothetical protein
SAG1100	210	conserved hypothetical protein
SAG1101	226	DNA repair protein RadC
SAG1102	377	membrane protein, putative
SAG1103	478	6-phospho-beta-glucosidase
SAG1104	204	platelet activating factor, putative
SAG1105	273	hydrolase, haloacid dehalogenase-like family
SAG1106	309	transcriptional regulator, AraC family, putative
SAG1107	510	voltage-gated chloride channel family protein
SAG1108	357	spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein
SAG1109	258	spermidine/putrescine ABC transporter, permease protein
SAG1110	264	spermidine/putrescine ABC transporter, permease protein
SAG1111	384	spermidine/putrescine ABC transporter, ATP-binding protein
SAG1112	300	UDP-N-acetylenolpyruvoylglucosamine reductase
SAG1113	162	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
SAG1114	120	dihydroneopterin aldolase
SAG1115	267	dihydropteroate synthase
SAG1116	187	GTP cyclohydrolase I
SAG1117	420	folylpolyglutamate synthase
SAG1118	295	rarD protein
SAG1119	288	homoserine kinase
SAG1120	427	homoserine dehydrogenase
SAG1121	295	polysaccharide deacetylase family protein
SAG1122	515	transporter, BCCT family protein
SAG1123	34	hypothetical protein
SAG1124	458	aldehyde dehydrogenase family protein
SAG1125	335	membrane protein, putative
SAG1126	228	protein of unknown function
SAG1127	446	conserved domain protein
SAG1128	65	transcriptional regulator, Cro/CI family
SAG1129	36	hypothetical protein
SAG1130	49	hypothetical protein
SAG1131	164	thiol peroxidase
SAG1132	219	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1133	254	conserved hypothetical protein
SAG1134	213	transcriptional regulator, GntR family/potassioum uptake protein, TrkA family
SAG1135	183	gls24 protein, putative
SAG1136	65	conserved hypothetical protein
SAG1137	180	gls24 protein, putative
SAG1138	64	conserved hypothetical protein
SAG1139	193	conserved hypothetical protein
SAG1140	82	conserved hypothetical protein
SAG1141	112	conserved hypothetical protein
SAG1142	759	ATP-dependent DNA helicase PcrA
SAG1143	128	conserved hypothetical protein
SAG1144	441	uracil permease
SAG1145	448	sodium:alanine symporter family protein
SAG1146	411	cation efflux family protein
SAG1147	130	conserved hypothetical protein
SAG1148	231	membrane protein, putative
SAG1149	207	lipoprotein, putative
SAG1150	400	ribosomal protein S1
SAG1151	76	conserved hypothetical protein
SAG1152	340	branched-chain amino acid aminotransferase
SAG1153	819	DNA topoisomerase IV, A subunit
SAG1154	653	DNA topoisomerase IV, B subunit
SAG1155	212	membrane protein, putative
SAG1156	217	uracil-DNA glycosylase
SAG1157	161	conserved hypothetical protein
SAG1158	413	CMP-N-acetylneuraminic acid synthetase NeuA
SAG1159	209	neuD protein
SAG1160	384	UDP-N-acetylglucosamine-2-epimerase NeuC
SAG1161	341	N-acetyl neuramic acid synthetase NeuB
SAG1162	466	polysaccharide biosynthesis protein CpsL
SAG1163	318	polysaccharide biosynthesis protein CpsK(V)
SAG1164	321	glycosyl transferase CpsJ(V)
SAG1165	327	glycosyl transferase CpsO(V)
SAG1166	295	glycosyl transferase CpsN(V)
SAG1167	241	polysaccharide biosynthesis protein CpsM(V)
SAG1168	364	polysaccharide biosynthesis protein cpsH(V)
SAG1169	163	glycosyl transferase CpsG(V)
SAG1170	149	polysaccharide biosynthesis protein CpsF
SAG1171	462	glycosyl transferase CpsE
SAG1172	229	cpsD protein
SAG1173	230	cpsC protein
SAG1174	243	capsular polysaccharide biosynthesis protein CpsB
SAG1175	485	capsular polysaccharide biosynthesis protein CpsA
SAG1176	290	transcriptional regulator, LysR family, putative
SAG1177	255	conserved hypothetical protein
SAG1178	236	purine nucleoside phosphorylase
SAG1179	418	voltage-gated chloride channel family protein, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1180	269	purine nucleoside phosphorylase
SAG1181	135	arsenate reductase
SAG1182	403	phosphopentomutase
SAG1183	223	ribose 5-phosphate isomerase
SAG1184	236	conserved hypothetical protein
SAG1185	262	tributyrin esterase
SAG1186	553	metallo-beta-lactamase superfamily protein
SAG1187	253	ABC transporter, ATP-binding protein
SAG1188	287	ABC transporter, permease protein
SAG1189	334	conserved hypothetical protein
SAG1190	551	adherence and virulence protein A
SAG1191	239	alpha-acetolactate decarboxylase
SAG1192	560	acetolactate synthase, catabolic
SAG1193	408	TPR domain protein
SAG1194	396	membrane protein, putative
SAG1195	153	MutT/nudix family protein
SAG1196	160	mutator MutT protein
SAG1197	1072	hyaluronidase
SAG1198	348	dTDP-glucose 4,6-dehydratase
SAG1199	197	dTDP-4-dehydrorhamnose 3,5-epimerase
SAG1200	289	glucose-1-phosphate thymidylyltransferase
SAG1201	367	iminodiacetate oxidase, putative
SAG1202	262	conserved hypothetical protein TIGR00486
SAG1203	227	conserved hypothetical protein
SAG1204	226	DNA replication protein DnaD, putative
SAG1205	172	adenine phosphoribosyltransferase
SAG1206	854	conserved domain protein
SAG1207	32	hypothetical protein
SAG1208	732	single-stranded-DNA-specific exonuclease RecJ
SAG1209	253	oxidoreductase, short chain dehydrogenase/reductase family
SAG1210	309	metallo-beta-lactamase superfamily protein
SAG1211	215	conserved hypothetical protein
SAG1212	412	GTP-binding protein HflX
SAG1213	296	tRNA delta(2)-isopentenylpyrophosphate transferase
SAG1214	58	hypothetical protein
SAG1215	305	exfoliative toxin A, putative
SAG1216	1252	pullulanase, putative
SAG1217	NA	conserved hypothetical protein, authentic frameshift
SAG1218	194	conserved hypothetical protein
SAG1219	468	peptidase, M20/M25/M40 family
SAG1220	200	nitroreductase family protein
SAG1221	NA	glycerophosphoryl diester phosphodiesterase, putative, authentic point mutation
SAG1222	593	excinuclease ABC, C subunit
SAG1223	255	conserved hypothetical protein
SAG1224	446	MATE efflux family protein
SAG1225	136	conserved hypothetical protein
SAG1226	165	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1227	198	protein of unknown function
SAG1228	96	ISSdy1, transposase OrfA
SAG1229	259	ISSdy1, transposase OrfB
SAG1230	96	conserved hypothetical protein
SAG1231	NA	transposase OrfB, IS3 family, degenerate
SAG1232	77	transposase OrfB, IS3 family, truncation
SAG1233	822	streptococcal histidine triad family protein
SAG1234	306	laminin-binding surface protein
SAG1235	425	GBSi1, group II intron, maturase
SAG1236	NA	C5a peptidase, authentic frameshift
SAG1237	444	hypothetical protein
SAG1238	202	hypothetical protein
SAG1239	76	conserved hypothetical protein
SAG1240	125	conserved hypothetical protein, truncation
SAG1241	91	transposase OrfA, IS3 family
SAG1242	67	transposase OrfB, IS3 family, truncation
SAG1243	96	ISSdy1, transposase OrfA
SAG1244	259	ISSdy1, transposase OrfB
SAG1245	38	hypothetical protein
SAG1246	389	hypothetical protein
SAG1247	399	site-specific recombinase, phage integrase family
SAG1248	75	conserved hypothetical protein
SAG1249	74	transcriptional regulator, Cro/CI family
SAG1250	621	Tn5252, relaxase
SAG1251	121	Tn5252, Orf 9 protein
SAG1252	120	Tn5252, Orf 10 protein
SAG1253	435	transposase, ISL3 family
SAG1254	546	mercuric reductase
SAG1255	130	mercuric resistance operon regulatory protein MerR
SAG1256	142	IS861, transposase OrfB, truncation
SAG1257	709	cation-transporting ATPase, E1-E2 family
SAG1258	122	cadmium efflux system accessory protein
SAG1259	99	conserved hypothetical protein
SAG1260	262	hypothetical protein
SAG1261	198	conserved hypothetical protein
SAG1262	695	cation-transporting ATPase, E1-E2 family
SAG1263	NA	conserved domain protein, authentic frameshift
SAG1264	148	transcriptional repressor CopY, putative
SAG1265	206	cadmium resistance transporter, putative
SAG1266	152	hypothetical protein
SAG1267	108	hypothetical protein
SAG1268	230	repressor protein, putative
SAG1269	44	hypothetical protein
SAG1270	471	ImpB/MucB/SamB family protein
SAG1271	116	conserved hypothetical protein
SAG1272	102	conserved hypothetical protein
SAG1273	118	conserved hypothetical protein
SAG1274	129	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1275	75	hypothetical protein
SAG1276	358	conserved hypothetical protein
SAG1277	163	hypothetical protein
SAG1278	96	hypothetical protein
SAG1279	99	conserved domain protein
SAG1280	2274	SNF2 family protein
SAG1281	183	hypothetical protein
SAG1282	63	calcium-binding protein, putative
SAG1283	1631	agglutinin receptor
SAG1284	196	abortive infection protein AbiGI
SAG1285	281	abortive infection protein AbiGII
SAG1286	933	Tn5252, Orf28
SAG1287	776	Tn5252, Orf26
SAG1288	NA	Tn5252, Orf25, degenerate
SAG1289	284	Tn5252, Orf23
SAG1290	80	hypothetical protein
SAG1291	605	Tn5252, Orf 21 protein, internal deletion
SAG1292	162	hypothetical protein
SAG1293	194	protease, putative
SAG1294	77	conserved hypothetical protein
SAG1295	127	conserved hypothetical protein
SAG1296	142	conserved hypothetical protein
SAG1297	451	C-5 cytosine-specific DNA methylase
SAG1298	31	hypothetical protein
SAG1299	272	conserved hypothetical protein
SAG1300	57	conserved hypothetical protein
SAG1301	121	ribosomal protein L7/L12
SAG1302	166	ribosomal protein L10
SAG1303	702	ATP-dependent Clp protease, ATP-binding subunit
SAG1304	32	hypothetical protein
SAG1305	314	homocysteine S-methyltransferase MmuM, putative
SAG1306	458	amino acid permease
SAG1307	216	hypothetical protein
SAG1308	167	hypothetical protein
SAG1309	30	hypothetical protein
SAG1310	182	transcriptional regulator, TetR family
SAG1311	198	GTP-binding protein
SAG1312	408	ATP-dependent Clp protease, ATP-binding subunit ClpX
SAG1313	56	conserved hypothetical protein
SAG1314	164	dihydrofolate reductase
SAG1315	279	thymidylate synthase
SAG1316	390	HMG-CoA synthase
SAG1317	427	3-hydroxy-3-methylglutaryl-CoA reductase
SAG1318	149	conserved hypothetical protein
SAG1319	214	hemolysin III, putative
SAG1320	304	conserved hypothetical protein TIGR00147
SAG1321	284	glutathione S-transferase family protein, putative
SAG1322	72	conserved domain protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1323	331	isopentenyl-diphosphate delta-isomerase
SAG1324	330	phosphomevalonate kinase
SAG1325	314	diphosphomevalonate decarboxylase
SAG1326	292	mevalonate kinase, putative
SAG1327	409	sensor histidine kinase
SAG1328	228	DNA-binding response regulator
SAG1329	208	GTP pyrophosphokinase family protein
SAG1330	68	hypothetical protein
SAG1331	979	R5 protein
SAG1332	146	transcriptional regulator, MarR family, putative
SAG1333	690	5'-nucleotidase family protein
SAG1334	136	polypeptide deformylase, putative
SAG1335	449	NADP-specific glutamate dehydrogenase
SAG1336	169	membrane protein, putative
SAG1337	589	ABC transporter, ATP-binding/permease protein
SAG1338	579	ABC transporter, ATP-binding/permease protein
SAG1339	157	acetyltransferase, GNAT family
SAG1340	622	ABC transporter, ATP-binding protein
SAG1341	402	polyA polymerase family protein
SAG1342	282	DegV family protein
SAG1343	126	protein of unknown function
SAG1344	177	hypothetical protein
SAG1345	164	conserved hypothetical protein
SAG1346	654	PTS system, fructose specific IIABC components
SAG1347	303	1-phosphofructokinase
SAG1348	247	lactose phosphotransferase system repressor
SAG1349	411	beta-lactam resistance factor
SAG1350	544	surface antigen-related protein
SAG1351	307	2-dehydropantoate 2-reductase, putative
SAG1352	356	regulatory protein, putative
SAG1353	330	pyridine nucleotide-disulphide oxidoreductase family protein
SAG1354	251	tRNA (guanine-N1)-methyltransferase
SAG1355	172	16S rRNA processing protein RimM
SAG1356	503	transcriptional regulator, RofA family
SAG1357	80	KH domain protein
SAG1358	90	ribosomal protein S16
SAG1359	415	permease, putative
SAG1360	236	ABC transporter, ATP-binding protein
SAG1361	414	conserved hypothetical protein
SAG1362	532	carbamoyl-phosphate synthase, large subunit, putative
SAG1363	356	carbamoyl-phosphate synthase, small subunit
SAG1364	173	pyrimidine operon regulatory protein
SAG1365	296	ribosomal large subunit pseudouridine synthase, RluD subfamily
SAG1366	154	lipoprotein signal peptidase
SAG1367	301	transcriptional regulator, LysR family
SAG1368	94	ribosomal protein L27
SAG1369	112	conserved hypothetical protein
SAG1370	104	ribosomal protein L21

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1371	392	conserved hypothetical protein
SAG1372	404	thiamine biosynthesis protein ThiI
SAG1373	381	cysteine desulphurase
SAG1374	150	conserved hypothetical protein
SAG1375	449	glutathione reductase
SAG1376	111	conserved hypothetical protein
SAG1377	388	chorismate synthase
SAG1378	355	3-dehydroquinate synthase
SAG1379	225	3-dehydroquinate dehydratase
SAG1380	385	conserved hypothetical protein
SAG1381	714	sulfatase
SAG1382	119	ribosomal protein L20
SAG1383	66	ribosomal protein L35
SAG1384	176	translation initiation factor IF-3
SAG1385	227	cytidylate kinase
SAG1386	174	conserved hypothetical protein
SAG1387	65	ferredoxin, 4Fe-4S
SAG1388	163	conserved hypothetical protein
SAG1389	406	peptidase T
SAG1390	544	polysaccharide biosynthesis protein, putative
SAG1391	484	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase
SAG1392	264	iron compound ABC transporter, ATP-binding protein
SAG1393	310	iron compound ABC transporter, substrate-binding protein
SAG1394	341	iron compound ABC transporter, permease protein
SAG1395	333	iron compound ABC transporter, permease protein
SAG1396	217	conserved hypothetical protein
SAG1397	311	inorganic pyrophosphatase, manganese-dependent
SAG1398	262	pyruvate formate-lyase-activating enzyme
SAG1399	444	CBS domain protein
SAG1400	188	conserved hypothetical protein
SAG1401	311	conserved hypothetical protein TIGR01212
SAG1402	213	PAP2 family protein
SAG1403	194	membrane protein, putative
SAG1404	308	cell wall surface anchor family protein
SAG1405	294	sortase family protein
SAG1406	293	sortase family protein
SAG1407	705	cell wall surface anchor family protein
SAG1408	901	cell wall surface anchor family protein
SAG1409	NA	rogB protein, authentic frameshift
SAG1410	379	glycosyl transferase, group 1 family protein
SAG1411	282	glycosyl transferase, group 2 family protein
SAG1412	474	polysaccharide biosynthesis protein
SAG1413	454	membrane protein, putative
SAG1414	308	glycosyl transferase, group 2 family protein
SAG1415	311	glycosyl transferase, group 2 family protein
SAG1416	352	nucleotide sugar dehydratase, putative
SAG1417	240	nucleotidyl transferase, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1418	274	polysaccharide biosynthesis protein, putative
SAG1419	577	lipoprotein, putative
SAG1420	117	conserved hypothetical protein
SAG1421	243	glycosyl transferase, group 2 family protein
SAG1422	313	glycosyl transferase, group 2 family protein
SAG1423	384	glycosyl transferase, putative
SAG1424	284	dTDP-4-dehydrorhamnose reductase
SAG1425	113	conserved hypothetical protein
SAG1426	369	RNA polymerase sigma-70 factor
SAG1427	602	DNA primase
SAG1428	125	large conductance mechanosensitive channel protein
SAG1429	58	ribosomal protein S21
SAG1430	167	conserved hypothetical protein
SAG1431	268	amino acid ABC transporter, amino acid-binding protein
SAG1432	347	ammonium transporter family protein
SAG1433	375	conserved hypothetical protein
SAG1434	328	rhodanese family protein
SAG1435	101	conserved hypothetical protein
SAG1436	457	glycerol-3-phosphate transporter, putative
SAG1437	55	hypothetical protein
SAG1438	754	glycogen phosphorylase
SAG1439	498	4-alpha-glucanotransferase
SAG1440	342	maltose operon repressor MalR, putative
SAG1441	415	maltose/maltodextrin ABC transporter, maltose/maltodextrin-binding protein
SAG1442	456	maltose ABC transporter, permease protein
SAG1443	278	maltose ABC transporter, permease protein
SAG1444	490	proton/peptide symporter family protein
SAG1445	NA	MutT/nudix family protein, authentic frameshift
SAG1446	62	hypothetical protein
SAG1447	441	conserved hypothetical protein
SAG1448	502	glycosyl transferase, group 1 family protein
SAG1449	795	preprotein translocase SecA subunit, putative
SAG1450	330	conserved domain protein
SAG1451	494	conserved hypothetical protein
SAG1452	514	conserved hypothetical protein
SAG1453	409	preprotein translocase SecY family protein
SAG1454	398	glycosyl transferase, putative
SAG1455	295	glycosyl transferase, group 2 family protein
SAG1456	NA	glycosyl transferase, family 8, degenerate
SAG1457	129	IS1381, transposase OrfB
SAG1458	127	IS1381, transposase OrfA
SAG1459	413	glycosyl transferase family 8
SAG1460	401	glycosyl transferase, family 8
SAG1461	335	conserved hypothetical protein
SAG1462	970	cell wall surface anchor family protein
SAG1463	NA	transcriptional regulator, RofA family, authentic point mutation
SAG1464	663	excinuclease ABC, B subunit

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1465	306	protease, putative
SAG1466	727	glutamine ABC transporter, glutamine-binding protein/permease protein
SAG1467	246	glutamine ABC transporter, ATP-binding protein, GlnQ putative
SAG1468	116	conserved hypothetical protein
SAG1469	52	conserved hypothetical protein
SAG1470	437	GTP-binding protein, GTP1/Obg family
SAG1471	42	conserved hypothetical protein
SAG1472	413	aminopeptidase PepS
SAG1473	192	cell wall surface anchor family protein
SAG1474	680	amidase family protein
SAG1475	240	ribosomal small subunit pseudouridine synthase A
SAG1476	280	oxidoreductase, aldo/keto reductase family
SAG1477	224	nitroreductase family protein
SAG1478	130	lactoylglutathione lyase
SAG1479	308	glycosyl transferase, group 2 family protein
SAG1480	462	amino acid permease
SAG1481	155	SsrA-binding protein
SAG1482	801	exoribonuclease, VacB/Rnb family
SAG1483	78	preprotein translocase, SecG subunit
SAG1484	48	ribosomal protein L33
SAG1485	389	multi-drug resistance protein
SAG1486	548	membrane protein, putative
SAG1487	233	ABC transporter, ATP binding protein
SAG1488	195	dephospho-CoA kinase
SAG1489	273	formamidopyrimidine-DNA glycosylase
SAG1490	282	transcriptional regulator, MutR family
SAG1491	530	hypothetical protein
SAG1492	58	hypothetical protein
SAG1493	66	hypothetical protein
SAG1494	32	hypothetical protein
SAG1495	81	CAAX amino terminal protease family protein
SAG1496	110	hypothetical protein
SAG1497	37	hypothetical protein
SAG1498	133	hypothetical protein
SAG1499	299	GTP-binding protein Era
SAG1500	132	diacylglycerol kinase
SAG1501	161	conserved hypothetical protein TIGR00043
SAG1502	268	tetracenomycin polyketide synthesis O-methyltransferase TcmP, putative
SAG1503	39	hypothetical protein
SAG1504	38	hypothetical protein
SAG1505	158	MutT/nudix family protein
SAG1506	267	hypothetical protein
SAG1507	345	PhoH family protein
SAG1508	590	67 kDa Myosin-crossreactive streptococcal antigen
SAG1509	71	conserved hypothetical protein
SAG1510	169	peptide methionine sulfoxide reductase

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1511	284	conserved hypothetical protein
SAG1512	185	ribosome recycling factor
SAG1513	242	uridylate kinase
SAG1514	226	peptide ABC transporter, ATP-binding protein
SAG1515	262	peptide ABC transporter, ATP-binding protein
SAG1516	255	peptide ABC transporter, permease protein
SAG1517	314	peptide ABC transporter, permease protein
SAG1518	538	peptide ABC transporter, peptide-binding protein
SAG1519	229	ribosomal protein L1
SAG1520	141	ribosomal protein L11
SAG1521	388	transposase, IS30 family, putative
SAG1522	460	transporter, major facilitator family
SAG1523	404	peptidase, M20/M25/M40 family
SAG1524	294	transcriptional regulator, LysR family
SAG1525	117	conserved hypothetical protein
SAG1526	178	IS861, transposase OrfA
SAG1527	277	IS861, transposase OrfB
SAG1528	571	chorismate binding enzyme
SAG1529	816	FtsK/SpoIIIE family protein
SAG1530	267	peptidyl-prolyl cis-trans isomerase, cyclophilin-type
SAG1531	277	manganese ABC transporter, permease protein
SAG1532	238	manganese ABC transporter, ATP-binding protein
SAG1533	308	manganese ABC transporter, manganese-binding adhesion liprotein
SAG1534	215	iron-dependent transcriptional regulator
SAG1535	229	5-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase
SAG1536	89	conserved hypothetical protein
SAG1537	184	MutT/nudix family protein
SAG1538	459	UDP-N-acetylglucosamine pyrophosphorylase
SAG1539	31	hypothetical protein
SAG1540	137	conserved hypothetical protein
SAG1541	125	glyoxalase family protein
SAG1542	318	oxidoreductase, Gfo/Idh/MocA family
SAG1543	NA	conserved hypothetical protein, authentic frameshift
SAG1544	232	gluconate 5-dehydrogenase, putative
SAG1545	78	conserved hypothetical protein
SAG1546	82	conserved hypothetical protein
SAG1547	166	acetyltransferase, GNAT family
SAG1548	422	glycosyl transferase, group 2 family protein
SAG1549	127	IS1381, transposase OrfA
SAG1550	129	IS1381, transposase OrfB
SAG1551	67	hypothetical protein
SAG1552	719	conserved hypothetical protein
SAG1553	477	hypothetical protein
SAG1554	225	hypothetical protein
SAG1555	231	hypothetical protein
SAG1556	445	branched-chain amino acid transport system II carrier protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1557	665	methionyl-tRNA synthetase
SAG1558	291	tellurite resistance protein TehB
SAG1559	231	membrane protein, putative
SAG1560	40	hypothetical protein
SAG1561	405	PTS system, IIC component, putative
SAG1562	280	conserved hypothetical protein
SAG1563	275	exodeoxyribonuclease
SAG1564	118	conserved hypothetical protein
SAG1565	158	methylated-DNA--protein-cysteine S-methyltransferase
SAG1566	393	D-isomer specific 2-hydroxyacid dehydrogenase family protein
SAG1567	182	acetyltransferase, GNAT family
SAG1568	NA	phosphoserine aminotransferase, authentic frameshift
SAG1569	211	copper homeostasis protein CutC, putative
SAG1570	34	conserved hypothetical protein
SAG1571	53	hypothetical protein
SAG1572	287	tetrapyrrole methylase family protein
SAG1573	108	conserved hypothetical protein
SAG1574	287	DNA polymerase III, delta prime subunit, putative
SAG1575	211	thymidylate kinase
SAG1576	267	transposase, IS30 family, putative, truncation
SAG1577	219	AcuB family protein
SAG1578	236	branched-chain amino acid ABC transporter, ATP-binding protein
SAG1579	254	branched-chain amino acid ABC transporter, ATP-binding protein
SAG1580	317	branched-chain amino acid ABC transporter, permease protein
SAG1581	289	branched-chain amino acid ABC transporter, permease protein
SAG1582	388	branched-chain amino acid ABC transporter, amino acid-binding protein
SAG1583	81	conserved hypothetical protein
SAG1584	377	IS1548, transposase
SAG1585	196	ATP-dependent Clp protease, proteolytic subunit ClpP
SAG1586	209	uracil phosphoribosyltransferase
SAG1587	389	aminotransferase, class I
SAG1588	182	RNA methyltransferase, TrmH family, group 2
SAG1589	450	amino acid permease, putative
SAG1590	449	potassium uptake protein, Trk family
SAG1591	475	cation uptake protein, Trk family
SAG1592	83	conserved hypothetical protein TIGR00278
SAG1593	240	ribosomal large subunit pseudouridine synthase B
SAG1594	194	conserved hypothetical protein TIGR00281
SAG1595	235	conserved hypothetical protein
SAG1596	246	integrase/recombinase, phage integrase family
SAG1597	157	CBS domain protein
SAG1598	173	conserved hypothetical protein
SAG1599	324	HAM1 protein
SAG1600	264	glutamate racemase
SAG1601	79	conserved hypothetical protein
SAG1602	180	membrane protein, putative
SAG1603	173	transcriptional regulator, biotin repressor family

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1604	229	membrane protein, putative
SAG1605	167	conserved hypothetical protein
SAG1606	247	RNA methyltransferase, TrmH family
SAG1607	92	acylphosphatase
SAG1608	310	lipoprotein, putative
SAG1609	221	amino acid ABC transporter, permease protein
SAG1610	285	amino acid ABC transporter, substrate-binding protein
SAG1611	486	amidase family protein
SAG1612	160	transcription elongation factor GreA
SAG1613	600	conserved hypothetical protein
SAG1614	167	acetyltransferase, GNAT family
SAG1615	443	UDP-N-acetylmuramate--alanine ligase
SAG1616	205	conserved hypothetical protein
SAG1617	32	hypothetical protein
SAG1618	1032	Snf2 family protein
SAG1619	377	IS1548, transposase
SAG1620	436	phosphoglycerate dehydrogenase-related protein
SAG1621	300	primosomal protein DnaI
SAG1622	391	conserved hypothetical protein
SAG1623	159	conserved hypothetical protein TIGR00244
SAG1624	501	sensor histidine kinase CsrS
SAG1625	229	DNA-binding response regulator CsrR
SAG1626	177	conserved hypothetical protein
SAG1627	296	heat shock protein HtpX
SAG1628	184	lemA protein
SAG1629	237	glucose-inhibited division protein B
SAG1630	459	sodium transport family protein
SAG1631	223	potassium uptake protein, Trk family, putative
SAG1632	276	cobalt transport family protein
SAG1633	558	ABC transporter, ATP-binding protein
SAG1634	212	conserved hypothetical protein
SAG1635	402	sodium:dicarboxylate symporter family protein
SAG1636	455	branched-chain amino acid transport system II carrier protein
SAG1637	351	alcohol dehydrogenase, zinc-containing
SAG1638	230	ABC transporter, permease protein
SAG1639	356	ABC transporter, ATP-binding protein
SAG1640	458	peptidase, M20/M25/M40 family
SAG1641	274	YaeC family protein
SAG1642	277	ABC transporter, substrate-binding protein
SAG1643	229	glutamine amidotransferase, class I
SAG1644	37	hypothetical protein
SAG1645	238	conserved hypothetical protein TIGR01033
SAG1646	32	hypothetical protein
SAG1647	328	dihydroxyacetone kinase family protein
SAG1648	178	transcriptional regulator, TetR family, putative
SAG1649	37	hypothetical protein
SAG1650	329	dihydroxyacetone kinase family protein
SAG1651	192	dihydroxyacetone kinase family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1652	124	conserved hypothetical protein
SAG1653	237	glycerol uptake facilitator protein
SAG1654	134	conserved hypothetical protein
SAG1655	237	transcriptional regulator, MerR family
SAG1656	369	conserved hypothetical protein
SAG1657	83	hypothetical protein
SAG1658	244	conserved hypothetical protein
SAG1659	118	iojap-related protein
SAG1660	173	isochorismatase family protein
SAG1661	195	conserved hypothetical protein TIGR00488
SAG1662	210	conserved hypothetical protein TIGR00482
SAG1663	105	conserved hypothetical protein TIGR00253
SAG1664	372	GTP-binding protein
SAG1665	177	hydrolase, haloacid dehalogenase-like family
SAG1666	304	membrane protein, putative
SAG1667	480	glutamyl-tRNA(Gln) amidotransferase, B subunit
SAG1668	488	glutamyl-tRNA(Gln) amidotransferase, A subunit
SAG1669	100	glutamyl-tRNA(Gln) amidotransferase, C subunit
SAG1670	881	pyruvate phosphate dikinase
SAG1671	276	protein of unknown function
SAG1672	170	CBS domain protein
SAG1673	321	3-hydroxyacyl-CoA dehydrogenase family protein
SAG1674	182	isochorismatase family protein
SAG1675	261	transcriptional regulator CodY, putative
SAG1676	403	aminotransferase, class I
SAG1677	150	conserved hypothetical protein
SAG1678	460	hydrolase, haloacid dehalogenase-like family
SAG1679	320	asparaginase family protein
SAG1680	292	shikimate 5-dehydrogenase
SAG1681	304	oxidoreductase, aldo/keto reductase family
SAG1682	671	ATP-dependent DNA helicase RecG
SAG1683	512	immunogenic secreted protein, putative
SAG1684	366	alanine racemase
SAG1685	119	holo-(acyl-carrier-protein) synthase
SAG1686	335	phospho-2-dehydro-3-deoxyheptonate aldolase
SAG1687	842	preprotein translocase, SecA subunit
SAG1688	315	mannose-6-phosphate isomerase, class I
SAG1689	293	fructokinase
SAG1690	639	PTS system, IIABC components
SAG1691	479	sucrose-6-phosphate hydrolase
SAG1692	320	sucrose operon repressor ScrR
SAG1693	144	N utilization substance protein B
SAG1694	129	conserved hypothetical protein
SAG1695	186	translation elongation factor P
SAG1696	38	hypothetical protein
SAG1697	48	hypothetical protein
SAG1698	99	conserved hypothetical protein
SAG1699	30	hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1700	76	hypothetical protein
SAG1701	56	hypothetical protein
SAG1702	41	hypothetical protein
SAG1703	54	hypothetical protein
SAG1704	150	cytidine/deoxycytidylate deaminase family protein
SAG1705	NA	peptidase, M24 family, authentic point mutation
SAG1706	238	conserved hypothetical protein
SAG1707	499	drug resistance transporter, EmrB/QacA family
SAG1708	38	hypothetical protein
SAG1709	942	excinuclease ABC, A subunit
SAG1710	223	conserved hypothetical protein
SAG1711	314	magnesium transporter, CorA family
SAG1712	79	ribosomal protein S18
SAG1713	163	single-strand binding protein
SAG1714	95	ribosomal protein S6
SAG1715	374	A/G-specific adenine glycosylase
SAG1716	197	transcriptional regulator, Cro/CI family
SAG1717	104	thioredoxin
SAG1718	166	PAP2 family protein
SAG1719	779	MutS2 family protein
SAG1720	180	conserved hypothetical protein
SAG1721	103	conserved hypothetical protein
SAG1722	297	ribonuclease HIII
SAG1723	197	signal peptidase I
SAG1724	806	helicase, putative
SAG1725	160	conserved hypothetical protein
SAG1726	364	DNA-damage-inducible protein P
SAG1727	770	formate acetyltransferase
SAG1728	124	FMN-binding protein
SAG1729	309	conserved hypothetical protein
SAG1730	251	conserved hypothetical protein
SAG1731	298	membrane protein, putative
SAG1732	282	glycerol uptake facilitator protein, putative
SAG1733	150	universal stress protein family
SAG1734	400	transporter, putative
SAG1735	219	transcriptional regulator, Crp/Fnr family
SAG1736	761	X-pro dipeptidyl-peptidase
SAG1737	119	hypothetical protein
SAG1738	326	polyprenyl synthetase family protein
SAG1739	582	ABC transporter, ATP-binding protein CydC
SAG1740	572	ABC transporter, ATP-binding protein CydD
SAG1741	339	cytochrome d ubiquinol oxidase, subunit II
SAG1742	475	cytochrome d oxidase, subunit I
SAG1743	402	pyridine nucleotide-disulphide oxidoreductase family protein
SAG1744	299	prenyltransferase, UbiA family
SAG1745	148	hypothetical protein
SAG1746	35	hypothetical protein
SAG1747	99	conserved hypothetical protein TIGR00103

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1748	396	cyclopropane-fatty-acyl-phospholipid synthase
SAG1749	241	transcriptional regulator, merR family
SAG1750	195	exonuclease
SAG1751	178	conserved hypothetical protein
SAG1752	390	conserved hypothetical protein TIGR00275
SAG1753	260	conserved hypothetical protein
SAG1754	89	ribosomal protein S14
SAG1755	38	hypothetical protein
SAG1756	341	conserved hypothetical protein
SAG1757	336	O-sialoglycoprotein endopeptidase family protein
SAG1758	135	ribosomal-protein-alanine acetyltransferase, putative
SAG1759	230	protein of unknown function
SAG1760	76	conserved hypothetical protein
SAG1761	559	metallo-beta-lactamase superfamily protein
SAG1762	169	conserved hypothetical protein
SAG1763	448	glutamine synthetase, type I
SAG1764	123	transcriptional regulator GlnR
SAG1765	179	conserved hypothetical protein
SAG1766	398	phosphoglycerate kinase
SAG1767	289	acid phosphatase
SAG1768	336	glyceraldehyde 3-phosphate dehydrogenase
SAG1769	692	translation elongation factor G
SAG1770	156	ribosomal protein S7
SAG1771	137	ribosomal protein S12
SAG1772	270	pur operon repressor
SAG1773	313	HD domain protein
SAG1774	424	conserved hypothetical protein
SAG1775	210	conserved hypothetical protein
SAG1776	220	ribulose-phosphate 3-epimerase
SAG1777	290	conserved hypothetical protein TIGR00157
SAG1778	283	rRNA (guanine-N1-)-methyltransferase, putative
SAG1779	290	dimethyladenosine transferase
SAG1780	163	hypothetical protein
SAG1781	186	primase-related protein
SAG1782	260	deoxyribonuclease, TatD family
SAG1783	90	hypothetical protein
SAG1784	130	hypothetical protein
SAG1785	430	hypothetical protein
SAG1786	130	protein of unknown function
SAG1787	420	dltD protein
SAG1788	79	D-alanyl carrier protein
SAG1789	421	dltB protein
SAG1790	511	D-alanine-activating enzyme
SAG1791	395	sensor histidine kinase
SAG1792	224	DNA-binding response regulator
SAG1793	44	ribosomal protein L34
SAG1794	451	membrane protein, putative
SAG1795	388	transposase, IS30 family, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1796	575	amino acid ABC transporter, permease protein
SAG1797	407	amino acid ABC transporter, ATP-binding protein
SAG1798	39	hypothetical protein
SAG1799	792	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase
SAG1800	363	conserved hypothetical protein
SAG1801	559	transcriptional antiterminator, BglG family
SAG1802	253	conserved hypothetical protein
SAG1803	505	carbohydrate kinase, FGGY family
SAG1804	329	hypothetical protein
SAG1805	483	PTS system, IIC component, putative
SAG1806	318	glyoxylate reductase, NADH-dependent
SAG1807	339	hypothetical protein
SAG1808	327	sugar binding transcriptional regulator, LacI family
SAG1809	215	transaldolase family protein
SAG1810	238	carbohydrate isomerase, AraD/FucA family
SAG1811	287	hexulose-6-phosphate isomerase, putative
SAG1812	221	hexulose-6-phosphate synthase, putative
SAG1813	161	PTS system, IIA component
SAG1814	92	PTS system, IIB component
SAG1815	479	transport protein SgaT, putative
SAG1816	205	hypothetical protein
SAG1817	157	hypothetical protein
SAG1818	430	adenylosuccinate synthetase
SAG1819	340	perfringolysin O regulator protein
SAG1820	224	conserved hypothetical protein
SAG1821	750	glutamate--cysteine ligase/amino acid ligase, putative
SAG1822	272	protein of unknown function
SAG1823	418	protein of unknown function
SAG1824	291	chaperonin, 33 kDa
SAG1825	325	NifR3/Smm1 family protein
SAG1826	213	deoxynucleoside kinase family protein
SAG1827	163	phosphinothricin N-acetyltransferase
SAG1828	815	ATP-dependent Clp protease, ATP-binding subunit
SAG1829	154	transcriptional regulator CtsR
SAG1830	153	conserved hypothetical protein
SAG1831	346	translation elongation factor Ts
SAG1832	256	ribosomal protein S2
SAG1833	186	alkyl hydroperoxide reductase, subunit C
SAG1834	510	alkyl hydroperoxide reductase, subunit F
SAG1835	134	conserved hypothetical protein
SAG1836	61	conserved hypothetical protein
SAG1837	468	prophage LambdaSa2, lysin, putative
SAG1838	109	prophage LambdaSa2, holin, putative
SAG1839	136	conserved hypothetical protein
SAG1840	112	hypothetical protein
SAG1841	76	conserved domain protein
SAG1842	1224	prophage LambdaSa2, PblB, putative
SAG1843	240	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1844	911	conserved hypothetical protein
SAG1845	42	hypothetical protein
SAG1846	158	hypothetical protein
SAG1847	227	conserved hypothetical protein
SAG1848	114	conserved hypothetical protein
SAG1849	115	hypothetical protein
SAG1850	101	hypothetical protein
SAG1851	111	conserved domain protein
SAG1852	420	conserved domain protein
SAG1853	180	prophage LambdaSa2, protease, putative
SAG1854	380	conserved hypothetical protein
SAG1855	570	prophage LambdaSa2, terminase large subunit, putative
SAG1856	161	hypothetical protein
SAG1857	119	prophage LambdaSa2, HNH endonuclease family protein
SAG1858	95	hypothetical protein
SAG1859	180	prophage LambdaSa2, site-specific recombinase, phage integrase family
SAG1860	154	conserved hypothetical protein
SAG1861	119	prophage LambdaSa2, transcriptional regulator, Cro/CI family
SAG1862	86	hypothetical protein
SAG1863	138	prophage LambdaSa2, single-strand binding protein
SAG1864	68	hypothetical protein
SAG1865	74	conserved hypothetical protein
SAG1866	109	conserved hypothetical protein
SAG1867	163	conserved hypothetical protein
SAG1868	134	hypothetical protein
SAG1869	437	prophage LambdaSa2, type II DNA modification methyltransferase, putative
SAG1870	273	prophage LambdaSa2, DNA replication protein DnaC, putative
SAG1871	248	prophage LambdaSa2, bacteriophage replication protein/hypothetical protein, truncation/fusion
SAG1872	200	hypothetical protein
SAG1873	443	prophage LambdaSa2, replicative DNA helicase
SAG1874	87	hypothetical protein
SAG1875	94	conserved hypothetical protein
SAG1876	176	prophage LambdaSa2, HNH endonuclease family protein
SAG1877	236	prophage LambdaSa2, antirepressor protein, putative
SAG1878	102	conserved domain protein
SAG1879	156	hypothetical protein
SAG1880	54	hypothetical protein
SAG1881	51	hypothetical protein
SAG1882	120	prophage LambdaSa2, repressor protein, putative
SAG1883	128	conserved hypothetical protein
SAG1884	134	hypothetical protein
SAG1885	356	prophage LambdaSa2, site-specific recombinase, phage integrase family
SAG1886	32	hypothetical protein
SAG1887	689	Na+/H+ exchanger family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1888	78	hypothetical protein
SAG1889	317	microcin immunity protein MccF, putative
SAG1890	631	endopeptidase O
SAG1891	327	oxidoreductase, Gfo/Idh/MocA family
SAG1892	358	membrane protein, putative
SAG1893	59	hypothetical protein
SAG1894	214	cyclic nucleotide-binding domain protein
SAG1895	204	polypeptide deformylase
SAG1896	333	sugar binding transcriptional regulator RegR
SAG1897	634	conserved hypothetical protein
SAG1898	271	PTS system, IID component
SAG1899	288	PTS system, IIC component
SAG1900	164	PTS system, IIB component
SAG1901	398	glucuronyl hydrolase
SAG1902	144	PTS system, IIA component
SAG1903	34	hypothetical protein
SAG1904	270	oxidoreductase, short-chain dehydrogenase/reductase family
SAG1905	212	conserved hypothetical protein
SAG1906	335	carbohydrate kinase, PfkB family
SAG1907	212	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase
SAG1908	499	hypothetical protein
SAG1909	204	nitroreductase family protein
SAG1910	141	transcriptional regulator, MarR family
SAG1911	1468	DNA polymerase III, alpha subunit, Gram-positive type
SAG1912	194	N-acetylmuramoyl-L-alanine amidase, family 4 protein
SAG1913	617	prolyl-tRNA synthetase
SAG1914	419	membrane-associated zinc metalloprotease, putative
SAG1915	264	phosphatidate cytidylyltransferase
SAG1916	250	undecaprenyl diphosphate synthase
SAG1917	113	preprotein translocase, YajC subunit
SAG1918	114	bacteriocin transport accessory protein, putative
SAG1919	387	malate oxidoreductase
SAG1920	445	citrate carrier protein, CCS family
SAG1921	508	sensor histidine kinase
SAG1922	229	response regulator
SAG1923	331	UDP-glucose 4-epimerase
SAG1924	535	glucan 1,6-alpha-glucosidase
SAG1925	377	sugar ABC transporter, ATP-binding protein
SAG1926	283	helix-turn-helix domain protein, fis-type
SAG1927	298	lacX protein
SAG1928	325	tagatose 1,6-diphosphate aldolase
SAG1929	310	tagatose-6-phosphate kinase
SAG1930	171	galactose-6-phosphate isomerase, LacB subunit
SAG1931	141	galactose-6-phosphate isomerase, LacA subunit
SAG1932	816	neuraminidase-related protein
SAG1933	482	PTS system, IIC component, putative
SAG1934	101	PTS system, IIB component, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1935	157	PTS system, IIA component, putative
SAG1936	258	lactose phosphotransferase system repressor
SAG1937	NA	streptococcal histidine triad family protein, degenerate
SAG1938	307	adhesion lipoprotein
SAG1939	147	protein of unknown function TIGR00256
SAG1940	738	GTP pyrophosphokinase family protein
SAG1941	800	2`,3`-cyclic-nucleotide 2`-phosphodiesterase
SAG1942	151	nrdI protein
SAG1943	345	conserved hypothetical protein
SAG1944	165	conserved hypothetical protein
SAG1945	345	iron ABC transporter, iron-binding protein
SAG1946	257	DNA-binding response regulator
SAG1947	549	conserved hypothetical protein
SAG1948	275	PTS system, IID component
SAG1949	269	PTS system, IIC component
SAG1950	163	PTS system, IIB component
SAG1951	141	PTS system, IIA component, putative
SAG1952	353	membrane protein, putative
SAG1953	60	hypothetical protein
SAG1954	384	membrane protein, putative
SAG1955	282	ABC transporter, ATP-binding protein
SAG1956	96	conserved hypothetical protein, truncation
SAG1957	250	response regulator
SAG1958	276	conserved hypothetical protein
SAG1959	727	PTS system, IIABC components
SAG1960	551	sensor histidine kinase
SAG1961	225	phosphate regulon response regulator PhoB
SAG1962	218	phosphate transport system regulatory protein PhoU, putative
SAG1963	253	phosphate ABC transporter, ATP-binding protein
SAG1964	292	phosphate ABC transporter, permease protein
SAG1965	281	phosphate ABC transporter, permease protein
SAG1966	293	hemolysin precursor, putative
SAG1967	195	hypothetical protein
SAG1968	246	conserved hypothetical protein TIGR00046
SAG1969	317	ribosomal protein L11 methyltransferase
SAG1970	102	conserved hypothetical protein
SAG1971	41	hypothetical protein
SAG1972	238	transcriptional regulator, MerR family
SAG1973	156	acetyltransferase, GNAT family
SAG1974	152	MutT/nudix family protein
SAG1975	47	hypothetical protein
SAG1976	156	conserved hypothetical protein
SAG1977	163	acetyltransferase, GNAT family
SAG1978	422	ATPase, AAA family
SAG1979	253	membrane protein, putative
SAG1980	300	ABC transporter, ATP-binding protein
SAG1981	68	hypothetical protein
SAG1982	359	transcriptional regulator, Cro/CI family

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1983	105	conserved hypothetical protein
SAG1984	188	conserved hypothetical protein TIGR00730
SAG1985	51	hypothetical protein
SAG1986	375	site-specific recombinase, phage integrase family
SAG1987	61	conserved hypothetical protein
SAG1988	342	conserved hypothetical protein
SAG1989	139	hypothetical protein
SAG1990	127	hypothetical protein
SAG1991	204	transcriptional regulator, Cro/CI family
SAG1992	518	protein of unknown function
SAG1993	373	site-specific recombinase, phage integrase family
SAG1994	108	conserved hypothetical protein
SAG1995	210	hypothetical protein
SAG1996	263	cell wall surface anchor family protein, putative
SAG1997	182	hypothetical protein
SAG1998	457	hypothetical protein
SAG1999	47	hypothetical protein
SAG2000	666	membrane protein, putative
SAG2001	756	conjugal transfer protein, interruption-C
SAG2002	129	IS1381, transposase OrfB
SAG2003	127	IS1381, transposase OrfA
SAG2004	67	conjugal transfer protein, interruption-N
SAG2005	136	conserved hypothetical protein
SAG2006	88	conserved hypothetical protein
SAG2007	317	conserved hypothetical protein
SAG2008	84	conserved hypothetical protein
SAG2009	88	conserved hypothetical protein
SAG2010	157	hypothetical protein
SAG2011	160	conserved hypothetical protein
SAG2012	90	hypothetical protein
SAG2013	189	hypothetical protein
SAG2014	449	hypothetical protein
SAG2015	99	transcriptional regulator, Cro/CI family
SAG2016	125	hypothetical protein
SAG2017	429	transcriptional regulator, Cro/CI family
SAG2018	553	FtsK/SpoIIIE family protein
SAG2019	153	hypothetical protein
SAG2020	98	hypothetical protein
SAG2021	826	cell wall surface anchor family protein
SAG2022	417	transposase, ISL3 family
SAG2023	546	mercuric reductase
SAG2024	130	mercuric resistance operon regulatory protein MerR
SAG2025	522	Mn2+/Fe2+ transporter, NRAMP family
SAG2026	240	membrane protein, putative
SAG2027	205	ABC transporter, ATP-binding protein
SAG2028	36	conserved hypothetical protein
SAG2029	284	streptomycin resistance protein
SAG2030	130	hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG2031	202	hypothetical protein
SAG2032	111	conserved hypothetical protein
SAG2033	162	acetyltransferase, GNAT family
SAG2034	247	membrane protein, putative
SAG2035	300	ABC transporter, ATP-binding protein
SAG2036	68	hypothetical protein
SAG2037	358	transcriptional regulator, Cro/CI family
SAG2038	204	PAP2 family protein
SAG2039	98	conserved hypothetical protein
SAG2040	186	conserved hypothetical protein TIGR00730
SAG2041	287	protease, putative
SAG2042	100	rhodanese family protein
SAG2043	255	cAMP factor
SAG2044	62	hypothetical protein
SAG2045	179	DNA topology modulation protein FlaR, putative
SAG2046	361	glycerol dehydrogenase, putative
SAG2047	235	conserved hypothetical protein
SAG2048	614	5-methyltetrahydrofolate--homocysteine methyltransferase, putative
SAG2049	745	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
SAG2050	107	conserved hypothetical protein
SAG2051	230	branched-chain amino acid transport protein AzlC, putative
SAG2052	41	hypothetical protein
SAG2053	1570	serine protease, subtilase family, putative
SAG2054	228	DNA-binding response regulator
SAG2055	462	sensor histidine kinase
SAG2056	202	chromosome assembly-related protein
SAG2057	833	leucyl-tRNA synthetase
SAG2058	415	major facilitator family protein
SAG2059	281	protein of unknown function
SAG2060	398	glycosyl transferase, family 8
SAG2061	401	glycosyl transferase, family 8
SAG2062	179	transcription antitermination protein NusG
SAG2063	630	pathogenicity protein, putative
SAG2064	57	preprotein translocase, SecE subunit, putative
SAG2065	50	ribosomal protein L33
SAG2066	773	penicillin-binding protein 2A
SAG2067	294	ribosomal large subunit pseudouridine synthase, RluD subfamily
SAG2068	546	conserved hypothetical protein
SAG2069	403	phosphopentomutase
SAG2070	223	deoxyribose-phosphate aldolase
SAG2071	400	Na+ dependent nucleoside transporter
SAG2072	259	uridine phosphorylase
SAG2073	245	transcriptional regulator, GntR family
SAG2074	540	60 kda chaperonin
SAG2075	94	chaperonin, 10 kDa
SAG2076	267	ABC transporter, ATP-binding protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG2077	298	ABC transporter, permease protein
SAG2078	320	protein of unknown function/lipoprotein, putative
SAG2079	265	hydrolase, haloacid dehalogenase-like family
SAG2080	286	glyoxalase family protein
SAG2081	243	conserved hypothetical protein
SAG2082	205	anaerobic ribonucleoside-triphosphate reductase activating protein
SAG2083	163	acetyltransferase, GNAT family
SAG2084	310	virulence factor MviM, putative
SAG2085	47	conserved hypothetical protein
SAG2086	723	anaerobic ribonucleoside-triphosphate reductase
SAG2087	495	membrane protein, putative
SAG2088	40	hypothetical protein
SAG2089	105	conserved hypothetical protein
SAG2090	136	conserved hypothetical protein TIGR00250
SAG2091	88	conserved hypothetical protein
SAG2092	132	conserved hypothetical protein
SAG2093	379	recA protein
SAG2094	NA	competence/damage-inducible protein CinA, authentic frameshift
SAG2095	183	DNA-3-methyladenine glycosylase I
SAG2096	196	Holliday junction DNA helicase RuvA
SAG2097	418	transporter, putative
SAG2098	659	DNA mismatch repair protein HexB
SAG2099	33	hypothetical protein
SAG2100	67	cold shock protein, CSD family
SAG2101	858	DNA mismatch repair protein HexA
SAG2102	145	arginine repressor ArgR, putative
SAG2103	563	arginyl-tRNA synthetase
SAG2104	102	conserved hypothetical protein
SAG2105	290	conserved hypothetical protein
SAG2106	314	conserved hypothetical protein
SAG2107	583	aspartyl-tRNA synthetase
SAG2108	426	histidyl-tRNA synthetase
SAG2109	60	ribosomal protein L32
SAG2110	49	ribosomal protein L33
SAG2111	173	conserved hypothetical protein
SAG2112	494	site-specific recombinase, phage integrase family
SAG2113	82	conserved hypothetical protein
SAG2114	342	conserved hypothetical protein
SAG2115	143	hypothetical protein
SAG2116	151	conserved hypothetical protein
SAG2117	71	hypothetical protein
SAG2118	306	transcriptional regulator, Cro/CI family
SAG2119	373	conserved domain protein
SAG2120	269	hypothetical protein
SAG2121	223	hypothetical protein
SAG2122	223	DNA-binding response regulator
SAG2123	454	sensor histidine kinase
SAG2124	517	membrane protein, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG2125	308	carbamate kinase
SAG2126	332	ornithine carbamoyltransferase
SAG2127	431	sensor histidine kinase
SAG2128	277	response regulator
SAG2129	240	amino acid ABC transporter, ATP-binding protein
SAG2130	504	amino acid ABC transporter, amino acid-binding protein/permease protein
SAG2131	847	membrane protein, putative
SAG2132	247	conserved hypothetical protein
SAG2133	118	conserved hypothetical protein
SAG2134	772	membrane protein, putative
SAG2135	179	transcriptional regulator, TetR family, putative
SAG2136	98	conserved hypothetical protein
SAG2137	203	ribosomal protein S4
SAG2138	95	conserved hypothetical protein
SAG2139	451	replicative DNA helicase
SAG2140	150	ribosomal protein L9
SAG2141	660	DHH family protein
SAG2142	613	glucose inhibited division protein A
SAG2143	203	membrane protein, putative
SAG2144	373	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
SAG2145	222	L-serine dehydratase, iron-sulfur-dependent, beta subunit
SAG2146	290	L-serine dehydratase, iron-sulfur-dependent, alpha subunit
SAG2147	234	protein of unknown function/lipoprotein, putative
SAG2148	179	LysM domain protein
SAG2149	264	cobalt transport family protein
SAG2150	280	ABC transporter, ATP-binding protein
SAG2151	279	ABC transporter, ATP-binding protein
SAG2152	180	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
SAG2153	427	peptidase, M16 family
SAG2154	414	conserved hypothetical protein
SAG2155	117	conserved hypothetical protein
SAG2156	369	recF protein
SAG2157	278	transporter, putative
SAG2158	220	transcriptional regulator, Cro/CI family
SAG2159	493	inosine-5'-monophosphate dehydrogenase
SAG2160	161	transcriptional regulator, ArgR family
SAG2161	226	transcriptional regulator, Crp/Fnr family
SAG2162	234	conserved hypothetical protein
SAG2163	410	arginine deiminase
SAG2164	136	acetyltransferase, GNAT family
SAG2165	337	ornithine carbamoyltransferase
SAG2166	475	arginine/ornithine antiporter
SAG2167	318	carbamate kinase
SAG2168	341	tryptophanyl-tRNA synthetase
SAG2169	230	membrane protein, putative
SAG2170	290	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG2171	539	ABC transporter, ATP-binding protein
SAG2172	859	ABC transporter, permease protein, putative
SAG2173	159	conserved hypothetical protein TIGR00246
SAG2174	409	serine protease
SAG2175	257	partitioning protein, ParB family

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo-protein	Other	Western blot	FACS	GBS specific	Annotation
SAG0017	447	+							pcsB
SAG0031	299	+							peptidase, M23/M37 family
SAG0032	434	+				+	+		group B streptococcal surface immunogenic protein
SAG0034	438	+		+		+	+		sugar ABC transporter, sugar-binding protein
SAG0051	126	+				+	+		MORN motif family protein
SAG0079	212				+	+	+		adenylate kinase
SAG0086	85			+				+	lipoprotein, putative
SAG0093	250	+				+	+		D-alanyl-D-alanine carboxypeptidase family protein
SAG0094	191	+							N-acetylmuramoyl-L-alanine amidase, family 4 protein
SAG0108	308	+							conserved hypothetical protein
SAG0114	322	+		+					ribose ABC transporter, periplasmic D-ribose-binding protein
SAG0124	356	+							sensor histidine kinase
SAG0132	294	+				+	+		SPFH domain/Band 7 family protein
SAG0134	96	+						+	hypothetical protein
SAG0146	395	+							penicillin-binding protein 4, putative
SAG0147	411	+							D-alanyl-D-alanine carboxypeptidase family protein
SAG0148	551			+		+	-		oligopeptide ABC transporter, substrate-binding protein, putative
SAG0166	123	+							conserved domain protein
SAG0176	94	+							conserved hypothetical protein
SAG0187	542	+		+		+	+		oligopeptide ABC transporter, oligopeptide-binding protein
SAG0206	60			+				+	lipoprotein, putative
SAG0213	39	+						+	hypothetical protein
SAG0231	135	+							hypothetical protein
SAG0242	308			+		+	-		amino acid ABC transporter, amino acid-binding protein
SAG0245	152			+		+	-	+	protein of unknown function/lipoprotein, putative
SAG0255	315	+							conserved hypothetical protein
SAG0257	53			+				+	lipoprotein, putative
SAG0265	235	+				+	-	+	conserved hypothetical protein
SAG0290	270	+				+	+		ABC transporter, substrate-binding protein
SAG0298	750	+							penicillin-binding protein 1A

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo-protein	Other	Western blot	FACS	GBS specific	Annotation
SAG0306	535	+							KH domain protein
SAG0321	339	+							sensor histidine kinase, putative
SAG0329	106	+							PTS system, cellobiose-specific IIB component
SAG0368	435	+				+	+		protein of unknown function
SAG0371	167	+						+	hypothetical protein
SAG0383	334	+		+		+	-		protein of unknown function/lipoprotein, putative
SAG0392	521	+	+			+	+		cell wall surface anchor family protein
SAG0394	345				+				sensor histidine kinase
SAG0405	347	+		+		+	+		protein of unknown function/lipoprotein, putative
SAG0406	299	+							UTP-glucose-1-phosphate uridylyltransferase
SAG0407	338	+							glycerol-3-phosphate dehydrogenase (NAD(P)+)
SAG0416	1233	+	+			+	+		protease, putative
SAG0421	1055		+			+	-		cell wall surface anchor family protein
SAG0433	1389		+						surface protein Rib
SAG0437	123			+					lipoprotein, putative
SAG0451	149	+		+				+	bacteriocin transport accessory protein,putative
SAG0455	357	+							conserved hypothetical protein
SAG0472	126	+				+	-		rhodanese-like family protein
SAG0482	84	+							YGGT family protein
SAG0499	275				+				hemolysin A
SAG0503	279	+				+	+		lipase/acylhydrolase
SAG0504	200	+							conserved hypothetical protein
SAG0506	65	+						+	hypothetical protein
SAG0521	236	+							carboxymethylenebutenolidase-related protein
SAG0535	506	+				+	+		zinc ABC transporter, zinc-binding adhesion liprotein
SAG0596	670				+				prophage LambdaSa1, pblA protein, internal deletion
SAG0603	111				+				conserved hypothetical protein
SAG0604	239				+				prophage LambdaSa1, lysin, putative
SAG0617	439				+				sensor histidine kinase VncS
SAG0624	574	+							septation ring formation regulator EzrA, putative
SAG0629	354	+							conserved domain protein
SAG0635	245	+				+	-		acid phosphatase, class B
SAG0638	109	+							cell wall surface anchor family protein, interruption-N

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo-protein	Other	Western blot	FACS	GBS specific	Annotation
SAG0645	554		+			+	+		cell wall surface anchor family protein
SAG0646	307	+	+			+	-		cell wall surface anchor family protein
SAG0647	305	+							sortase family protein
SAG0649	890		+			+	+		cell wall surface anchor family protein, putative
SAG0658	383	+		+					lipoprotein, putative
SAG0675	171	+							putative secreted protein
SAG0676	885				+				proteinase, putative
SAG0677	1062		+						hypothetical protein
SAG0679	343	+		+		+	-		protein of unknown function
SAG0680	339	+				+	-		protein of unknown function
SAG0681	353	+							conserved domain protein
SAG0686	261	+				+	+		DNA-entry nuclease, putative
SAG0714	188	+						+	conserved hypothetical protein
SAG0717	266	+				+	+		amino acid ABC transporter, amino acid-binding protein
SAG0720	449				+				sensory box histidine kinase
SAG0738	132	+							conserved hypothetical protein
SAG0739	143	+							conserved hypothetical protein
SAG0742	428				+	+	+		peptidase, U32 family
SAG0755	282	+							peptidase, U32 family
SAG0757	129	+		+		+	-		protein of unknown function/lipoprotein, putative
SAG0764	230				+	+	+		phosphoglycerate mutase family protein
SAG0765	681	+							penicillin-binding protein 2b
SAG0771	512	+	+			+	+	+	cell wall surface anchor family protein
SAG0776	276	+		+					YaeC family protein, putative
SAG0777	528				+	+	+		ATP-dependent RNA helicase, DEAD/DEAH box family
SAG0785	330	+							conserved hypothetical protein
SAG0808	309	+		+		+	+		protease maturation protein, putative
SAG0824	417	+							polysaccharide deacetylase family protein
SAG0832	753	+				+	+		protein of unknown function
SAG0833	181	+						+	hypothetical protein
SAG0867	63	+							conserved hypothetical protein
SAG0868	285	+				+	-		DNA-entry nuclease
SAG0886	319	+				+	+		protein of unknown function

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo-protein	Other	Western blot	FACS	GBS specific	Annotation
SAG0904	56	+						+	hypothetical protein
SAG0907	877	+		+		+	-		protein of unknown function/lipoprotein, putative
SAG0926	333	+							Tn916, NLP/P60 family protein
SAG0942	185	+				+	+		signal peptidase I, putative
SAG0949	276	+		+		+	+		amino acid ABC transporter, amino acid-binding protein
SAG0954	349			+		+	-		protein of unknown function/lipoprotein, putative
SAG0961	247	+				+	-		sortase SrtA
SAG0963	320	+							conserved hypothetical protein
SAG0971	282	+		+		+	-		protein of unknown function/lipoprotein, putative
SAG0973	320	+						+	nisin-resistance protein, putative
SAG0977	312				+				sensor histidine kinase
SAG0979	553	+		+		+	-		ABC transporter, substrate-binding protein
SAG0984	437	+							sensor histidine kinase CiaH
SAG0992	286	+		+		+	+		phosphate ABC transporter, phosphate-binding protein
SAG1007	342	+		+		+	-		iron-compound ABC transporter, iron-compound-binding protein
SAG1014	190	+				-	-		conserved hypothetical protein
SAG1018	40			+				+	lipoprotein, putative
SAG1024	183	+		+					lipoprotein, putative
SAG1029	101	+							hypothetical protein
SAG1030	304	+				+	+		protein of unknown function
SAG1037	157	+						+	hypothetical protein
SAG1052	47		+					+	cell wall surface anchor family protein, putative
SAG1072	200	+							conserved hypothetical protein
SAG1094	278				+	+	+		conserved hypothetical protein
SAG1108	357	+				+	-		spermidine/putrescine ABC transporter, spermidine/putrescine-binding prot.
SAG1121	295	+							polysaccharide deacetylase family protein
SAG1126	228	+				+	+		protein of unknown function
SAG1127	446	+						+	conserved domain protein
SAG1130	49	+						+	hypothetical protein
SAG1138	64	+							conserved hypothetical protein
SAG1139	193	+							conserved hypothetical protein

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo-protein	Other	Western blot	FACS	GBS specific	Annotation
SAG1149	207	+		+					lipoprotein, putative
SAG1184	236	+							conserved hypothetical protein
SAG1186	553				+				metallo-beta-lactamase superfamily protein
SAG1189	334	+							conserved hypothetical protein
SAG1190	551				+				adherence and virulence protein A
SAG1197	1072	+							hyaluronidase
SAG1201	367	+							iminodiacetate oxidase, putative
SAG1206	854	+							conserved domain protein
SAG1214	58	+							hypothetical protein
SAG1216	1252		+			+	-		pullulanase, putative
SAG1227	198	+				+	-		protein of unknown function
SAG1233	822	+				+	-		streptococcal histidine triad family protein
SAG1234	306	+		+		+	+		laminin-binding surface protein
SAG1238	202	+							hypothetical protein
SAG1283	1631		+			+	+		agglutinin receptor
SAG1313	56	+							conserved hypothetical protein
SAG1327	409	+							sensor histidine kinase
SAG1331	979	+	+			+	+		R5 protein
SAG1333	690	+	+			+	+		5'-nucleotidase family protein
SAG1350	544	+							surface antigen-related protein
SAG1361	414	+							conserved hypothetical protein
SAG1371	392	+							conserved hypothetical protein
SAG1393	310			+					iron compound ABC transporter, substrate-binding protein
SAG1404	308	+	+			+	-		cell wall surface anchor family protein
SAG1405	294	+			+	+	+		sortase family protein
SAG1406	293	+							sortase family protein
SAG1407	705	+	+			+	+		cell wall surface anchor family protein
SAG1408	901		+						cell wall surface anchor family protein
SAG1419	577			+				+	lipoprotein, putative
SAG1431	268			+					amino acid ABC transporter, amino acid-binding protein
SAG1433	375	+							conserved hypothetical protein
SAG1441	415	+				+	+		maltose/maltodextrin ABC transporter, maltose/maltodextrin-binding protein

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo-protein	Other	Western blot	FACS	GBS specific	Annotation
SAG1462	970		+						cell wall surface anchor family protein
SAG1473	192	+	+					+	cell wall surface anchor family protein
SAG1474	680	+	+						amidase family protein
SAG1483	78	+							preprotein translocase, SecG subunit
SAG1488	195	+				+	+		dephospho-CoA kinase
SAG1491	530	+						+	hypothetical protein
SAG1508	590				+	+	-		67 kDa Myosin-crossreactive streptococcal antigen
SAG1518	538	+		+					peptide ABC transporter, peptide-binding protein
SAG1530	267	+		+		+	-		peptidyl-prolyl cis-trans isomerase, cyclophilin-type
SAG1533	308	+		+		+	-		manganese ABC transporter, manganese-binding adhesion liprotein
SAG1544	232	+							gluconate 5-dehydrogenase, putative
SAG1551	67	+						+	hypothetical protein
SAG1552	719	+							conserved hypothetical protein
SAG1553	477	+						+	hypothetical protein
SAG1562	280	+							conserved hypothetical protein
SAG1582	388	+		+		+	-		branched-chain amino acid ABC transporter, amino acid-binding protein
SAG1590	449				+	+	+		potassium uptake protein, Trk family
SAG1601	79	+							conserved hypothetical protein
SAG1610	285			+		+	-		amino acid ABC transporter, substrate-binding protein
SAG1618	1032				+	+	+		Snf2 family protein
SAG1624	501	+							sensor histidine kinase CsrS
SAG1628	184	+							lemA protein
SAG1631	223	+				+	-		potassium uptake protein, Trk family, putative
SAG1641	274	+				+	-		YaeC family protein
SAG1642	277	+		+		+	-		ABC transporter, substrate-binding protein
SAG1683	512	+							immunogenic secreted protein, putative
SAG1706	238	+							conserved hypothetical protein
SAG1745	148	+						+	hypothetical protein
SAG1752	390	+							conserved hypothetical protein TIGR00275
SAG1759	230				+	+	+		protein of unknown function
SAG1762	169	+							conserved hypothetical protein

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo-protein	Other	Western blot	FACS	GBS specific	Annotation
SAG1767	289	+		+					acid phosphatase
SAG1768	336				+	+	+		glyceraldehyde 3-phosphate dehydrogenase
SAG1774	424	+							conserved hypothetical protein
SAG1786	130	+				+	-		protein of unknown function
SAG1787	420	+							dltD protein
SAG1791	395	+							sensor histidine kinase
SAG1822	272	+				+	-		protein of unknown function
SAG1823	418				+	+	+		protein of unknown function
SAG1837	468				+				prophage LambdaSa2, lysin, putative
SAG1838	109	+							prophage LambdaSa2, holin, putative
SAG1839	136	+							conserved hypothetical protein
SAG1842	1224				+				prophage LambdaSa2, PblB, putative
SAG1912	194	+							N-acetylmuramoyl-L-alanine amidase, family 4 protein
SAG1921	508	+							sensor histidine kinase
SAG1932	816	+							neuraminidase-related protein
SAG1938	307	+		+		+	-		adhesion lipoprotein
SAG1941	800	+	+			+	-		2',3'-cyclic-nucleotide 2'-phosphodiesterase
SAG1945	345	+							iron ABC transporter, iron-binding protein
SAG1947	549				+				conserved hypothetical protein
SAG1960	551				+	+	+		sensor histidine kinase
SAG1966	293			+		+	-		hemolysin precursor, putative
SAG1996	263	+	+						cell wall surface anchor family protein, putative
SAG1997	182	+							hypothetical protein
SAG1998	457	+							hypothetical protein
SAG2021	826		+						cell wall surface anchor family protein
SAG2043	255	+							cAMP factor
SAG2053	1570	+	+						serine protease, subtilase family, putative
SAG2055	462				+				sensor histidine kinase
SAG2056	202	+						+	chromosome assembly-related protein
SAG2063	630	+	+						pathogenicity protein, putative
SAG2078	320	+		+		+	-		protein of unknown function/lipoprotein, putative
SAG2094		+				+	+		competence/damage-inducible protein CinA, authentic frameshift

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo-protein	Other	Western blot	FACS	GBS specific	Annotation
SAG2121	223	+						+	hypothetical protein
SAG2123	454	+							sensor histidine kinase
SAG2141	660	+				+	-		DHH family protein
SAG2147	234	+		+		+	+		protein of unknown function/lipoprotein, putative
SAG2148	179	+							LysM domain protein
SAG2174	409	+							serine protease
SAG0013	428	+				+	-		protein of unknown function

Table 3

ORF	Annotation
SAG0038	conserved hypothetical protein
SAG0048	transcriptional regulator Cro/CI family
SAG0091	transcriptional regulator ComX1 putative
SAG0137	conserved hypothetical protein
SAG0686	DNA-entry nuclease putative
SAG0770	membrane protein putative
SAG0868	DNA-entry nuclease
SAG1143	conserved hypothetical protein
SAG1233	streptococcal histidine triad family protein
SAG1596	integrase/recombinase phage integrase family
SAG1616	conserved hypothetical protein
SAG1721	conserved hypothetical protein.

Table 4: Probable recently duplicated genes

Probable recently duplicated genes are indicated on the same line and are separated by a semicolon.

SAG0148 oligopeptide ABC transporter, substrate-binding protein, putative; SAG0979 ABC transporter, substrate-binding protein

SAG0151 oligopeptide ABC transporter, ATP-binding protein; SAG1515 peptide ABC transporter, ATP-binding protein

SAG0195 IS1548, transposase; SAG0693 IS1548, transposase; SAG0760 IS1548, transposase; SAG0945 IS1548, transposase; SAG1584 IS1548, transposase; SAG1619 IS1548, transposase

SAG0230 conserved hypothetical protein; SAG1039 conserved hypothetical protein

SAG0233 hypothetical protein; SAG1785 hypothetical protein

SAG0261 IS1381, transposase OrfB; SAG0542 IS1381, transposase OrfA; SAG0543 IS1381, transposase OrfB; SAG0966 IS1381, transposase OrfB; SAG1457 IS1381, transposase OrfB; SAG1550 IS1381, transposase OrfB; SAG2002 IS1381, transposase OrfB

SAG0262 IS1381, transposase OrfA; SAG0965 IS1381, transposase OrfA; SAG1549 IS1381, transposase OrfA; SAG1458 IS1381, transposase OrfA; SAG2003 IS1381, transposase OrfA

SAG0383 protein of unknown function/lipoprotein, putative; SAG0785 conserved hypothetical protein

SAG0405 protein of unknown function/lipoprotein, putative; SAG0954 protein of unknown function/lipoprotein, putative

SAG0417 glycosyl transferase, group 2 family protein; SAG1422 glycosyl transferase, group 2 family protein

SAG0429 oxidoreductase, aldo/keto reductase family; SAG1476 oxidoreductase, aldo/keto reductase family

Table 4: Probable recently duplicated genes

SAG0432 transcriptional regulator, AraC family; SAG0644 transcriptional regulator, AraC family

SAG0434 transposase, IS256 family, truncation; SAG0448 transposase, IS256 family

SAG0438 bacteriophage L54a, integrase, truncation; SAG1986 site-specific recombinase, phage integrase family; SAG1989 hypothetical protein; SAG1993 site-specific recombinase, phage integrase family; SAG2115 hypothetical protein

SAG0442 acetyltransferase, GNAT family; SAG0443 acetyltransferase, GNAT family

SAG0447 magnesium transporter, CorA family; SAG0875 magnesium transporter, CorA family, putative

SAG0508 beta-lactam resistance factor; SAG1349 beta-lactam resistance factor

SAG0566 prophage LambdaSa1, single-strand binding protein; SAG1713 single-strand binding protein; SAG1863 prophage LambdaSa2, single-strand binding protein

SAG0603 conserved hypothetical protein; SAG1838 prophage LambdaSa2, holin, putative

SAG0604 prophage LambdaSa1, lysin, putative; SAG1837 prophage LambdaSa2, lysin, putative

SAG0618 transposase OrfB, IS3 family, truncation; SAG0639 transposase OrfB, IS3 family; SAG1232 transposase OrfB, IS3 family, truncation; SAG1242 transposase OrfB, IS3 family, truncation

SAG0640 transposase OrfA, IS3 family; SAG1241 transposase OrfA, IS3 family

SAG0646 cell wall surface anchor family protein; SAG1404 cell wall surface anchor family protein

Table 4: Probable recently duplicated genes

SAG0647 sortase family protein; SAG0648 sortase family protein; SAG0650 sortase family protein

SAG0649 cell wall surface anchor family protein, putative; SAG1408 cell wall surface anchor family protein

SAG0676 proteinase, putative; SAG2053 serine protease, subtilase family, putative

SAG0679 protein of unknown function; SAG0680 protein of unknown function; SAG0681 conserved domain protein

SAG1002 protease, putative; SAG1465 protease, putative

SAG1025 hypothetical protein; SAG1033 FtsK/SpoIIIE family protein

SAG1067 IS861, transposase OrfA; SAG1526 IS861, transposase OrfA

SAG1068 IS861, transposase OrfB; SAG1256 IS861, transposase OrfB, truncation; SAG1527 IS861, transposase OrfB

SAG1140 conserved hypothetical protein; SAG1141 conserved hypothetical protein

SAG1164 glycosyl transferase CpsJ(V); SAG1165 glycosyl transferase CpsO(V)

SAG1182 phosphopentomutase; SAG2069 phosphopentomutase

SAG1225 conserved hypothetical protein; SAG1540 conserved hypothetical protein

SAG1228 ISSdy1, transposase OrfA; SAG1243 ISSdy1, transposase OrfA

SAG1229 ISSdy1, transposase OrfB; SAG1244 ISSdy1, transposase OrfB

SAG1253 transposase, ISL3 family; SAG2022 transposase, ISL3 family

Table 4: Probable recently duplicated genes

SAG1254 mercuric reductase; SAG2023 mercuric reductase

SAG1255 mercuric resistance operon regulatory protein MerR; SAG2024 mercuric resistance operon regulatory protein MerR

SAG1259 conserved hypothetical protein; SAG1272 conserved hypothetical protein

SAG1283 agglutinin receptor; SAG2021 cell wall surface anchor family protein

SAG1297 C-5 cytosine-specific DNA methylase; SAG1869 prophage LambdaSa2, type II DNA modification methyltransferase, putative

SAG1405 sortase family protein; SAG1406 sortase family protein

SAG1414 glycosyl transferase, group 2 family protein; SAG1415 glycosyl transferase, group 2 family protein

SAG1456 glycosyl transferase, family 8, degenerate; SAG2060 glycosyl transferase, family 8

SAG1521 transposase, IS30 family, putative; SAG1576 transposase, IS30 family, putative, truncation; SAG1795 transposase, IS30 family, putative

SAG1655 transcriptional regulator, MerR family; SAG1972 transcriptional regulator, MerR family

SAG1979 membrane protein, putative; SAG2034 membrane protein, putative

SAG1980 ABC transporter, ATP-binding protein; SAG2035 ABC transporter, ATP-binding protein

SAG1982 transcriptional regulator, Cro/CI family; SAG2037 transcriptional regulator, Cro/CI family

SAG1983 conserved hypothetical protein; SAG2039 conserved hypothetical protein

Table 4: Probable recently duplicated genes

SAG1984 conserved hypothetical protein TIGR00730; SAG2040 conserved hypothetical protein TIGR00730

SAG1988 conserved hypothetical protein; SAG2114 conserved hypothetical protein

Table 5

Strain	Source	Capsular serotype	Reference
090	Lancefield	Ia	
515	Houston	Ia	(1)
A909	Lancefield	Ia	(2)
Davis	Channing	Ia	
DK1	Houston	Ia	
DK8	Houston	Ia	
H36b	Lancefield	Ib	(2)
(S7) 7357b	Channing	Ib	(3)
18RS21	Lancefield	II	(4)
DK21	Houston	II	
COH1	Seattle	III	(5)
COH31	Seattle	III	(6)
D136C	Lancefield	III	(4)
M781	Houston	III	(7)
M732	Houston	III	(8)
1169NT1	Atlanta	V	(9)
2603V/R	Italy	V	This study
CJB111	Houston	V	(10)
JM9130013	Japan	VIII	(11)
SMU014	Japan	VIII	(11)
CJB110	Houston	Nontypeable	(12)

Table 5

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Table 6

Cluster 1

SAG0230	conserved hypothetical protein
SAG0231	hypothetical protein
SAG0232	hypothetical protein
SAG0233	hypothetical protein
SAG0234	hypothetical protein
SAG0235	hypothetical protein

Cluster 2

SAG0222	conserved domain protein
SAG0223	conserved hypothetical protein, fusion
SAG0225	hypothetical protein
SAG0226	recombination protein
SAG0227	hypothetical protein
SAG0228	conserved hypothetical protein
SAG0229	conserved hypothetical protein

Cluster 3

SAG0634	hypothetical protein
SAG0635	acid phosphatase, class B
SAG0636	conserved hypothetical protein
SAG0638	cell wall surface anchor family protein, interruption-N
SAG0640	transposase OrfA, IS3 family

Table 6

SAG0642	hypothetical protein
SAG0643	chaperonin, 33 kDa, degenerate
SAG0644	transcriptional regulator, AraC family
SAG0645	cell wall surface anchor family protein
SAG0646	cell wall surface anchor family protein
SAG0647	sortase family protein
SAG0648	sortase family protein
SAG0649	cell wall surface anchor family protein, putative
SAG0650	sortase family protein
SAG0651	protein of unknown function

Cluster 4

SAG1898	PTS system, IID component
SAG1899	PTS system, IIC component
SAG1900	PTS system, IIB component
SAG1901	glucuronyl hydrolase
SAG1902	PTS system, IIA component
SAG1905	conserved hypothetical protein
SAG1906	carbohydrate kinase, PfkB family

Cluster 5

SAG0247	hypothetical protein
SAG0248	hypothetical protein

Table 6

SAG0249	hypothetical protein
SAG0674	hypothetical protein
SAG0675	putative secreted protein
SAG0676	proteinase, putative
SAG0677	hypothetical protein
SAG0680	protein of unknown function
SAG0681	conserved domain protein
SAG0684	ABC transporter, ATP-binding protein
SAG1698	conserved hypothetical protein

Cluster 6

SAG0261	IS1381, transposase OrfB
SAG0262	IS1381, transposase OrfA
SAG0965	IS1381, transposase OrfA
SAG0966	IS1381, transposase OrfB
SAG2002	IS1381, transposase OrfB

Cluster 7

SAG1027	conserved hypothetical protein
SAG1028	hypothetical protein
SAG1029	hypothetical protein
SAG1030	protein of unknown function
SAG1031	conserved domain protein

Table 6

SAG1032	conserved hypothetical protein

Cluster 8

SAG1253	transposase, ISL3 family
SAG1254	mercuric reductase
SAG1255	mercuric resistance operon regulatory protein MerR
SAG2022	transposase, ISL3 family
SAG2023	mercuric reductase
SAG2024	mercuric resistance operon regulatory protein MerR

Cluster 9

SAG1993	site-specific recombinase, phage integrase family
SAG1994	conserved hypothetical protein
SAG1995	hypothetical protein
SAG1996	cell wall surface anchor family protein, putative
SAG1997	hypothetical protein
SAG1998	hypothetical protein
SAG2000	membrane protein, putative
SAG2001	conjugal transfer protein, interruption-C
SAG2007	conserved hypothetical protein
SAG2008	conserved hypothetical protein
SAG2009	conserved hypothetical protein
SAG2010	hypothetical protein

Table 6

SAG2011	conserved hypothetical protein
SAG2012	hypothetical protein
SAG2016	hypothetical protein
SAG2017	transcriptional regulator, Cro/CI family
SAG2025	Mn2+/Fe2+ transporter, NRAMP family

Cluster 10

SAG1039	conserved hypothetical protein
SAG1447	conserved hypothetical protein
SAG1448	glycosyl transferase, group 1 family protein
SAG1449	preprotein translocase SecA subunit, putative
SAG1450	conserved domain protein
SAG1452	conserved hypothetical protein
SAG1453	preprotein translocase SecY family protein
SAG1454	glycosyl transferase, putative
SAG1455	glycosyl transferase, group 2 family protein
SAG1456	glycosyl transferase, family 8, degenerate
SAG1459	glycosyl transferase family 8
SAG1460	glycosyl transferase, family 8
SAG1461	conserved hypothetical protein
SAG1462	cell wall surface anchor family protein
SAG1463	transcriptional regulator, RofA family, authentic point mutation
SAG1469	conserved hypothetical protein

Table 6

SAG1471	conserved hypothetical protein
SAG1933	PTS system, IIC component, putative

Cluster 11

SAG0009	hypothetical protein
SAG0120	hypothetical protein
SAG0157	deoxyribonuclease-related protein, degenerate
SAG0186	hypothetical protein
SAG0216	hypothetical protein
SAG0236	hypothetical protein
SAG0307	hypothetical protein
SAG0308	ABC transporter, ATP-binding protein
SAG0311	DNA-binding response regulator, authentic point mutation
SAG0518	peptide chain release factor 2, programmed frameshift
SAG0553	hypothetical protein
SAG0555	prophage LambdaSa1, antirepressor, putative
SAG0564	conserved hypothetical protein
SAG0579	conserved hypothetical protein
SAG0580	conserved hypothetical protein, truncation
SAG0611	transposase, degenerate
SAG0637	transcriptional regulator, TetR family, putative, authentic frameshift
SAG0641	Tn5252, Orf 10 protein, degenerate
SAG0652	Tn5252, Orf 28 protein, degenerate

Table 6

SAG0655	conserved hypothetical protein
SAG0678	endopeptidase O, degenerate
SAG0683	transmembrane protein Vexp3, putative, degenerate
SAG0855	glycogen biosynthesis protein GlgD, authentic frameshift
SAG0898	hypothetical protein
SAG0899	hypothetical protein
SAG0901	hypothetical protein
SAG0902	hypothetical protein
SAG0903	hypothetical protein
SAG0917	Tn916, hypothetical protein
SAG0920	Tn916, hypothetical protein
SAG0922	Tn916, hypothetical protein
SAG0924	Tn916, tetM leader peptide
SAG0928	Tn916, hypothetical protein, authentic frameshift
SAG0936	Tn916, hypothetical protein
SAG0943	hypothetical protein
SAG0972	conserved hypothetical protein, authentic frameshift
SAG1023	hypothetical protein
SAG1080	hypothetical protein
SAG1123	hypothetical protein
SAG1129	hypothetical protein
SAG1136	conserved hypothetical protein
SAG1217	conserved hypothetical protein, authentic frameshift

Table 6

SAG1231	transposase OrfB, IS3 family, degenerate
SAG1242	transposase OrfB, IS3 family, truncation
SAG1309	hypothetical protein
SAG1331	R5 protein
SAG1437	hypothetical protein
SAG1445	MutT/nudix family protein, authentic frameshift
SAG1484	ribosomal protein L33
SAG1493	hypothetical protein
SAG1539	hypothetical protein
SAG1543	conserved hypothetical protein, authentic frameshift
SAG1560	hypothetical protein
SAG1568	phosphoserine aminotransferase, authentic frameshift
SAG1570	conserved hypothetical protein
SAG1601	conserved hypothetical protein
SAG1644	hypothetical protein
SAG1646	hypothetical protein
SAG1699	hypothetical protein
SAG1705	peptidase, M24 family, authentic point mutation
SAG1708	hypothetical protein
SAG1857	prophage LambdaSa2, HNH endonuclease family protein
SAG1864	hypothetical protein
SAG1868	hypothetical protein

Table 6

SAG1869	prophage LambdaSa2, type II DNA modification methyltransferase, putative
SAG1872	hypothetical protein
SAG1874	hypothetical protein
SAG1876	prophage LambdaSa2, HNH endonuclease family protein
SAG1878	conserved domain protein
SAG1881	hypothetical protein
SAG1883	conserved hypothetical protein
SAG1886	hypothetical protein
SAG1903	hypothetical protein
SAG1937	streptococcal histidine triad family protein, degenerate
SAG1971	hypothetical protein
SAG1979	membrane protein, putative
SAG1980	ABC transporter, ATP-binding protein
SAG1981	hypothetical protein
SAG1982	transcriptional regulator, Cro/CI family
SAG1983	conserved hypothetical protein
SAG1984	conserved hypothetical protein TIGR00730
SAG1985	hypothetical protein
SAG1991	transcriptional regulator, Cro/CI family
SAG1992	protein of unknown function
SAG1999	hypothetical protein
SAG2004	conjugal transfer protein, interruption-N

Table 6

SAG2039	conserved hypothetical protein
SAG2044	hypothetical protein
SAG2052	hypothetical protein
SAG2065	ribosomal protein L33
SAG2094	competence/damage-inducible protein CinA, authentic frameshift
SAG2099	hypothetical protein

Cluster 12

SAG1164	glycosyl transferase CpsJ(V)
SAG1165	glycosyl transferase CpsO(V)
SAG1166	glycosyl transferase CpsN(V)
SAG1167	polysaccharide biosynthesis protein CpsM(V)
SAG1168	polysaccharide biosynthesis protein cpsH(V)

Cluster 13

SAG0581	conserved hypothetical protein
SAG0582	conserved hypothetical protein
SAG0583	conserved hypothetical protein
SAG0585	conserved hypothetical protein
SAG0586	conserved hypothetical protein
SAG0587	prophage LambdaSa1, structural protein, putative
SAG0588	conserved hypothetical protein
SAG0589	conserved hypothetical protein

Table 6

SAG0590	conserved hypothetical protein
SAG0591	conserved hypothetical protein
SAG0593	prophage LambdaSa1, structural protein
SAG0594	conserved hypothetical protein
SAG0595	conserved hypothetical protein
SAG0596	prophage LambdaSa1, pblA protein, internal deletion

Cluster 14

SAG0915	Tn916, transposase
SAG0918	Tn916, hypothetical protein
SAG0919	Tn916, hypothetical protein
SAG0921	Tn916, transcriptional regulator, putative
SAG0925	Tn916, hypothetical protein
SAG0926	Tn916, NLP/P60 family protein
SAG0927	membrane protein, putative
SAG0929	Tn916, hypothetical protein
SAG0930	Tn916, hypothetical protein
SAG0931	Tn916, hypothetical protein
SAG0932	Tn916, transcriptional regulator, putative
SAG0933	Tn916, FtsK/SpoIIIE family protein
SAG0934	Tn916, hypothetical protein
SAG0935	Tn916, hypothetical protein
SAG0937	ABC transporter, ATP-binding protein, authentic frameshift

Table 6

Cluster 15

SAG1835	conserved hypothetical protein
SAG1837	prophage LambdaSa2, lysin, putative
SAG1839	conserved hypothetical protein
SAG1840	hypothetical protein
SAG1842	prophage LambdaSa2, PblB, putative
SAG1843	conserved hypothetical protein
SAG1844	conserved hypothetical protein
SAG1849	hypothetical protein
SAG1851	conserved domain protein
SAG1852	conserved domain protein
SAG1853	prophage LambdaSa2, protease, putative
SAG1854	conserved hypothetical protein
SAG1855	prophage LambdaSa2, terminase large subunit, putative
SAG1856	hypothetical protein
SAG1858	hypothetical protein
SAG1859	prophage LambdaSa2, site-specific recombinase, phage integrase family
SAG1860	conserved hypothetical protein
SAG1861	prophage LambdaSa2, transcriptional regulator, Cro/CI family
SAG1862	hypothetical protein
SAG1863	prophage LambdaSa2, single-strand binding protein
SAG1865	conserved hypothetical protein

Table 6

SAG1866	conserved hypothetical protein
SAG1867	conserved hypothetical protein
SAG1870	prophage LambdaSa2, DNA replication protein DnaC, putative
SAG1871	prophage LambdaSa2, bacteriophage replication protein/hypothetical protein, truncation/fusion
SAG1873	prophage LambdaSa2, replicative DNA helicase
SAG1877	prophage LambdaSa2, antirepressor protein, putative
SAG1879	hypothetical protein
SAG1882	prophage LambdaSa2, repressor protein, putative
SAG1884	hypothetical protein
SAG1885	prophage LambdaSa2, site-specific recombinase, phage integrase family

Cluster 16

SAG1247	site-specific recombinase, phage integrase family
SAG1250	Tn5252, relaxase
SAG1251	Tn5252, Orf 9 protein
SAG1252	Tn5252, Orf 10 protein
SAG1256	IS861, transposase OrfB, truncation
SAG1257	cation-transporting ATPase, E1-E2 family
SAG1258	cadmium efflux system accessory protein
SAG1259	conserved hypothetical protein
SAG1260	hypothetical protein
SAG1261	conserved hypothetical protein

Table 6

SAG1262	cation-transporting ATPase, E1-E2 family
SAG1263	conserved domain protein, authentic frameshift
SAG1264	transcriptional repressor CopY, putative
SAG1265	cadmium resistance transporter, putative
SAG1266	hypothetical protein
SAG1267	hypothetical protein
SAG1268	repressor protein, putative
SAG1270	ImpB/MucB/SamB family protein
SAG1271	conserved hypothetical protein
SAG1272	conserved hypothetical protein
SAG1273	conserved hypothetical protein
SAG1274	conserved hypothetical protein
SAG1276	conserved hypothetical protein
SAG1277	hypothetical protein
SAG1278	hypothetical protein
SAG1279	conserved domain protein
SAG1280	SNF2 family protein
SAG1281	hypothetical protein
SAG1283	agglutinin receptor
SAG1284	abortive infection protein AbiGI
SAG1285	abortive infection protein AbiGII
SAG1286	Tn5252, Orf28
SAG1287	Tn5252, Orf26

Table 6

SAG1288	Tn5252, Orf25, degenerate
SAG1289	Tn5252, Orf23
SAG1290	hypothetical protein
SAG1291	Tn5252, Orf 21 protein, internal deletion
SAG1292	hypothetical protein
SAG1293	protease, putative
SAG1294	conserved hypothetical protein
SAG1295	conserved hypothetical protein
SAG1296	conserved hypothetical protein
SAG1297	C-5 cytosine-specific DNA methylase
SAG1299	conserved hypothetical protein
SAG1304	hypothetical protein

Table 7

Locus	**Annotation**
Housekeeping	
SAG0466	thiolase
SAG0471	glucokinase
SAG0492	amino acid ABC transporter, ATP-binding protein
SAG0767	D-alanine--D-alanine ligase
SAG1086	xanthine phosphoribosyltransferase
SAG1600	glutamate racemase
SAG1680	shikimate 5-dehydrogenase
SAG1723	signal peptidase I
Surface-exposed	
SAG0079	adenylate kinase
SAG0093	D-alanyl-D-alanine carboxypeptidase family protein
SAG0163	competence protein CglA
SAG0290	ABC transporter, substrate-binding protein
SAG0368	protein of unknown function
SAG0503	lipase/acylhydrolase
SAG1473	cell wall surface anchor family protein
SAG1552	conserved hypothetical protein
SAG1641	YaeC family protein
SAG2147	protein of unknown function/lipoprotein, putative
SAG2148	LysM domain protein

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx	Annotation
ORF00003	PcsB protein (pscB)
ORF00004	ribose-phosphate pyrophosphokinase (prsA)
ORF00005	aminotransferase, class I
ORF00006	recombination protein O
ORF00009	fatty acid/phospholipid synthesis protein PlsX (plsX)
ORF00011	phosphoribosylaminoimidazole-succinocarboxamide synthase (purC)
ORF00012	phosphoribosylformylglycinamidine synthase, putative
ORF00013	amidophosphoribosyltransferase (purF)
ORF00014	phosphoribosylformylglycinamidine cyclo-ligase (purM)
ORF00015	phosphoribosylglycinamide formyltransferase (purN)
ORF00020	group B streptococcal surface immunogenic protein
ORF00021	N-acetylmannosamine-6-P epimerase, putative
ORF00022	sugar ABC transporter, sugar-binding protein
ORF00023	sugar ABC transporter, permease protein
ORF00024	sugar ABC transporter, permease protein
ORF00026	conserved hypothetical protein
ORF00027	N-acetylneuraminate lyase, putative
ORF00028	expressed ROK family protein
ORF00030	phosphosugar-binding transcriptional regulator, RpiR family, putative
ORF00031	phosphoribosylamine--glycine ligase (purD)
ORF00032	phosphoribosylaminoimidazole carboxylase, catalytic subunit (purE)
ORF00033	phosphoribosylaminoimidazole carboxylase, ATPase subunit (purK)
ORF00036	adenylosuccinate lyase (purB)
ORF00037	transcriptional regulator, Cro/CI family
ORF00038	Holliday junction DNA helicase RuvB (ruvB)
ORF00039	phosphotyrosine protein phosphatase, low molecular weight
ORF00040	MORN motif family protein
ORF00041	membrane protein, putative
ORF00043	alcohol dehydrogenase, propanol-preferring (adhP)
ORF00045	MATE efflux family protein
ORF00046	ribosomal protein S10 (rpsJ)
ORF00047	ribosomal protein L3 (rplC)
ORF00048	ribosomal protein L4 (rplD)
ORF00049	ribosomal protein L23 (rplW)
ORF00050	ribosomal protein L2 (rplB)
ORF00052	ribosomal protein S19 (rpsS)
ORF00054	ribosomal protein L22 (rplV)
ORF00055	ribosomal protein S3 (rpsC)
ORF00056	ribosomal protein L16 (rplP)
ORF00058	ribosomal protein L29 (rpmC)
ORF00059	ribosomal protein S17 (rpsQ)
ORF00060	ribosomal protein L14 (rplN)
ORF00061	ribosomal protein L24 (rplX)
ORF00063	ribosomal protein L5 (rplE)
ORF00065	ribosomal protein S8 (rpsH)
ORF00066	ribosomal protein L6 (rplF)
ORF00068	ribosomal protein L18 (rplR)
ORF00069	ribosomal protein S5 (rpsE)
ORF00070	ribosomal protein L30 (rpmD)
ORF00071	ribosomal protein L15 (rplO)
ORF00072	preprotein translocase, SecY subunit
ORF00073	adenylate kinase (adk)
ORF00074	translation initiation factor IF-1 (infA)
ORF00075	ribosomal protein L36 (rpmJ)
ORF00077	ribosomal protein S13 (rpsM)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation
ORF00078 ribosomal protein S11 (rpsK)
ORF00080 DNA-directed RNA polymerase, alpha subunit (rpoA)
ORF00093 transcriptional regulator ComX1, putative
ORF00094 phosphoglycerate mutase family protein
ORF00097 heat-inducible transcription repressor HrcA (hrcA)
ORF00098 heat shock protein GrpE (grpE)
ORF00099 dnaK protein (dnaK)
ORF00100 dnaJ protein (dnaJ)
ORF00101 transcriptional regulator, GntR family
ORF00102 tRNA pseudouridine synthase A (truA)
ORF00103 phosphomethylpyrimidine kinase, putative
ORF00104 conserved hypothetical protein
ORF00105 conserved hypothetical protein
ORF00106 conserved hypothetical protein
ORF00107 trigger factor (tig)
ORF00108 DNA-directed RNA polymerase, delta subunit, putative
ORF00109 CTP synthase (pyrG)
ORF00111 deoxyuridine 5`-triphosphate nucleotidohydrolase (dut)
ORF00113 carbonic anhydrase-related protein
ORF00115 pyridine nucleotide-disulphide oxidoreductase family protein
ORF00116 glutamyl-tRNA synthetase (gltX)
ORF00119 ribose ABC transporter, ATP-binding protein (rbsA)
ORF00122 ribose operon repressor RbsR (rbsR)
ORF00125 ABC transporter, ATP-binding protein
ORF00126 DNA-binding response regulator
ORF00128 sensor histidine kinase
ORF00131 fructose-bisphosphate aldolase (fba)
ORF00132 L-2-hydroxyisocaproate dehydrogenase
ORF00133 ribosomal protein L28 (rpmB)
ORF00134 conserved hypothetical protein
ORF00135 DAK2 domain protein
ORF00136 expressed SPFH domain/Band 7 family protein
ORF00141 amino acid ABC transporter, ATP-binding protein
ORF00142 amino acid ABC transporter, amino acid-binding protein/permease protein
ORF00143 conserved hypothetical protein
ORF00145 undecaprenol kinase, putative
ORF00146 negative regulator of competence MecA, putative
ORF00149 ABC transporter, ATP-binding protein
ORF00150 conserved hypothetical protein
ORF00151 selenocysteine lyase (csdB)
ORF00152 NifU family protein
ORF00153 conserved hypothetical protein
ORF00155 D-alanyl-D-alanine carboxypeptidase
ORF00158 oligopeptide ABC transporter, permease protein
ORF00160 oligopeptide ABC transporter, ATP-binding protein
ORF00161 oligopeptide ABC transporter, ATP-binding protein
ORF00167 adc operon repressor AdcR (adcR)
ORF00168 zinc ABC transporter, ATP-binding protein
ORF00169 zinc ABC transporter, permease protein
ORF00172 tyrosyl-tRNA synthetase (tyrS)
ORF00173 penicillin-binding protein 1B, putative
ORF00174 DNA-directed RNA polymerase, beta subunit (rpoB)
ORF00176 DNA-directed RNA polymerase beta' subunit (rpoC)
ORF00178 conserved hypothetical protein
ORF00179 competence protein CglA (cglA)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx	Annotation
ORF00180	competence protein CglB (cglB)
ORF00181	conserved hypothetical protein
ORF00183	conserved hypothetical protein
ORF00184	acetate kinase (ackA)
ORF00190	pyrroline-5-carboxylate reductase (proC)
ORF00191	glutamyl-aminopeptidase (pepA)
ORF00198	single-strand binding protein (ssb)
ORF00211	PTS system, IIABC components
ORF00212	alpha amylase family protein
ORF00214	transcriptional antiterminator, BglG family
ORF00219	PTS system, IIC component, putative
ORF00224	ribosomal protein S15 (rpsO)
ORF00225	polyribonucleotide nucleotidyltransferase (pnp)
ORF00227	serine O-acetyltransferase (cysE)
ORF00229	cysteinyl-tRNA synthetase (cysS)
ORF00230	conserved hypothetical protein
ORF00231	RNA methyltransferase, TrmH family, group 3
ORF00233	DegV family protein
ORF00236	ribosomal protein L13 (rplM)
ORF00237	ribosomal protein S9 (rpsI)
ORF00261	transcriptional regulator MutR family
ORF00262	transporter, putative
ORF00263	amino acid ABC transporter, permease protein
ORF00264	amino acid ABC transporter, amino acid-binding protein
ORF00265	amino acid ABC transporter, permease protein
ORF00266	amino acid ABC transporter, ATP-binding protein
ORF00295	N-acetylglucosamine-6-phosphate deacetylase (nagA)
ORF00296	conserved hypothetical protein
ORF00297	glycyl-tRNA synthetase, alpha subunit (glyQ)
ORF00299	glycyl-tRNA synthetase, beta subunit (glyS)
ORF00300	conserved hypothetical protein
ORF00302	glycerol kinase (glpK)
ORF00303	alpha-glycerophosphate oxidase
ORF00304	glycerol uptake facilitator protein (glpF)
ORF00306	conserved hypothetical protein
ORF00307	transketolase (tkt)
ORF00309	ABC transporter, ATP-binding protein
ORF00310	membrane protein, putative
ORF00313	PTS system, IIBC components
ORF00314	glutamate 5-kinase (proB)
ORF00315	gamma-glutamyl phosphate reductase (proA)
ORF00316	conserved hypothetical protein TIGR00006
ORF00318	penicillin-binding protein 2X (pbpX)
ORF00319	phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY)
ORF00320	ATP-dependent RNA helicase, DEAD/DEAH box family
ORF00321	ABC transporter, substrate-binding protein
ORF00322	amino acid ABC transporter, permease protein
ORF00323	amino acid ABC transporter, ATP-binding protein
ORF00325	thioredoxin reductase (trxB)
ORF00326	conserved hypothetical protein
ORF00327	NAD synthetase (nadE)
ORF00328	aminopeptidase C (pepC)
ORF00329	penicillin-binding protein 1A (pbp1A)
ORF00330	recombination protein U (recU)
ORF00331	conserved hypothetical protein

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation
ORF00335 conserved hypothetical protein
ORF00336 conserved hypothetical protein
ORF00337 autoinducer-2 production protein LuxS (luxS)
ORF00338 KH domain protein
ORF00348 guanylate kinase (gmk)
ORF00349 DNA-directed RNA polymerase, omega subunit, putative
ORF00350 primosomal protein N' (priA)
ORF00351 methionyl-tRNA formyltransferase (fmt)
ORF00352 Sun protein (sun)
ORF00353 serine/threonine phosphatase, putative
ORF00354 serine/threonine protein kinase
ORF00355 conserved hypothetical protein
ORF00356 sensor histidine kinase, putative
ORF00358 DNA-binding response regulator
ORF00359 hydrolase, haloacid dehalogenase family/peptidyl-prolyl cis-trans isomerase, cyclophilin type
ORF00360 general stress protein, putative
ORF00361 pyruvate formate-lyase-activating enzyme (pflA)
ORF00362 transcriptional regulator, DeoR family
ORF00363 transcriptional regulator, putative
ORF00364 PTS system, cellobiose-specific IIA component (celC)
ORF00366 PTS system, cellobiose-specific IIB component (celA)
ORF00367 PTS system, cellobiose-specific IIC component (celB)
ORF00368 formate acetyltransferase (pflD)
ORF00369 transaldolase family protein
ORF00371 glycerol dehydrogenase (gldA)
ORF00372 cysteine synthase A (cysK)
ORF00373 conserved hypothetical protein TIGR00257
ORF00374 helicase, putative
ORF00375 competence protein F, putative
ORF00376 ribosomal subunit interface protein (yfiA)
ORF00385 enoyl-CoA hydratase/isomerase family protein
ORF00386 transcriptional regulator, MarR family
ORF00387 3-oxoacyl-(acyl-carrier-protein) synthase III (fabH)
ORF00388 acyl carrier protein (acpP)
ORF00390 enoyl-(acyl-carrier-protein) reductase II (fabK)
ORF00391 malonyl CoA-acyl carrier protein transacylase (fabD)
ORF00392 3-oxoacyl-[acyl-carrier protein] reductase (fabG)
ORF00393 3-oxoacyl-(acyl-carrier-protein) synthase II (fabF)
ORF00394 acetyl-CoA carboxylase, biotin carboxyl carrier protein (accB)
ORF00395 (3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase (fabZ)
ORF00396 acetyl-CoA carboxylase, biotin carboxylase (accC)
ORF00397 acetyl-CoA carboxylase, carboxyl transferase, beta subunit (accD)
ORF00398 acetyl-CoA carboxylase, carboxyl transferase, alpha subunit (accA)
ORF00400 seryl-tRNA synthetase (serS)
ORF00403 conserved hypothetical protein
ORF00404 PTS system, mannose-specific IID component
ORF00405 PTS system, mannose-specific IIC component (manM)
ORF00406 PTS system, mannose-specific IIAB components (manL)
ORF00407 hydrolase, haloacid dehalogenase-like family
ORF00410 xanthine/uracil permease family protein
ORF00411 conserved hypothetical protein TIGR00150, putative
ORF00412 acetyltransferase, GNAT family
ORF00413 expressed protein of unknown function
ORF00415 HIT family protein (hit)
ORF00419 ABC transporter, ATP-binding protein

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx	Annotation
ORF00421	ABC transporter, permease protein
ORF00422	conserved hypothetical protein
ORF00423	conserved hypothetical protein TIGR00091
ORF00424	conserved hypothetical protein, POINT MUTATION
ORF00425	N utilization substance protein A (nusA)
ORF00426	conserved hypothetical protein
ORF00427	ribosomal protein L7A family
ORF00428	translation initiation factor IF-2
ORF00429	ribosome-binding factor A (rbfA)
ORF00432	copper-transporter ATPase CopA
ORF00435	hydrolase, haloacid dehalogenase-like family
ORF00436	DNA polymerase I (polA)
ORF00437	CoA binding domain protein
ORF00440	DNA-binding response regulator
ORF00441	sensor histidine kinase
ORF00443	queuine tRNA-ribosyltransferase (tgt)
ORF00444	conserved hypothetical protein
ORF00449	glucose-6-phosphate isomerase (pgi)
ORF00451	rhomboid family protein
ORF00452	expressed putative lipoprotein
ORF00453	UTP-glucose-1-phosphate uridylyltransferase (galU)
ORF00454	glycerol-3-phosphate dehydrogenase (NAD(P)+) (gpsA)
ORF00455	ribonuclease P protein component (rnpA)
ORF00456	SpoIIIJ family protein
ORF00458	R3H domain protein
ORF00463	conserved hypothetical protein
ORF00464	RecX protein
ORF00465	RNA methyltransferase, TrmA family
ORF00470	ribonucleoside-diphosphate reductase 2, beta subunit (nrdF)
ORF00472	ribonucleoside-diphosphate reductase 2, alpha subunit (nrdE)
ORF00482	alcohol dehydrogenase, zinc-containing
ORF00483	oxidoreductase, aldo/keto reductase family
ORF00484	cation efflux system protein
ORF00485	transcriptional regulator, TetR family
ORF00496	conserved hypothetical protein
ORF00500	acetyltransferase, GNAT family
ORF00501	conserved hypothetical protein
ORF00502	valyl-tRNA synthetase (valS)
ORF00508	aspartate--ammonia ligase (asnA)
ORF00511	type II DNA modification methyltransferase, putative
ORF00513	phosphopantetheine adenylyltransferase (coaD)
ORF00515	conserved hypothetical protein
ORF00519	conserved hypothetical protein
ORF00520	conserved hypothetical protein TIGR00048
ORF00522	ABC transporter, ATP-binding/permease protein
ORF00523	ABC transporter, ATP-binding/permease protein
ORF00524	anthranilate synthase component II (trpG)
ORF00532	endonuclease III (nth)
ORF00534	conserved hypothetical protein
ORF00535	glucokinase (glk)
ORF00536	expressed protein with rhodanese domain
ORF00537	elongation factor Tu family protein
ORF00540	UDP-N-acetylmuramoylalanine--D-glutamate ligase (murD)
ORF00541	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (murG)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx	Annotation
ORF00542	cell division protein DivIB, putative
ORF00544	cell division protein FtsA (ftsA)
ORF00545	cell division protein FtsZ (ftsZ)
ORF00546	ylmE protein, putative
ORF00547	ylmF protein (ylmF)
ORF00549	ylmH protein (ylmH)
ORF00550	cell division protein DivIVA, putative
ORF00552	isoleucyl-tRNA synthetase (ileS)
ORF00553	conserved hypothetical protein
ORF00554	MutT/nudix family protein
ORF00555	ATP-dependent Clp protease, ATP-binding subunit
ORF00557	conserved hypothetical protein
ORF00558	amino acid ABC transporter, permease protein
ORF00559	amino acid ABC transporter, ATP-binding protein
ORF00560	phosphoglucomutase/phosphomannomutase family protein
ORF00562	methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase (folD)
ORF00564	exodeoxyribonuclease VII, large subunit (xseA)
ORF00566	geranyltranstransferase, putative
ORF00567	hemolysin A
ORF00570	DNA repair protein RecN (recN)
ORF00571	expressed DegV family protein
ORF00574	DNA-binding protein HU (hup)
ORF00576	dihydroorotate dehydrogenase A (pyrDA)
ORF00577	beta-lactam resistance factor (fibB)
ORF00578	beta-lactam resistance factor (fibA)
ORF00579	murM protein, putative
ORF00580	hydrolase, haloacid dehalogenase-like family
ORF00581	HD domain protein
ORF00582	conserved hypothetical protein
ORF00583	cation-transporting ATPase, E1-E2 family
ORF00588	cell division ABC transporter, ATP-binding protein FtsE (ftsE)
ORF00589	cell division ABC transporter, permease protein FtsX (ftsX)
ORF00591	metallo-beta-lactamase superfamily protein
ORF00593	DNA polymerase III, epsilon subunit/ATP-dependent helicase DinG
ORF00595	aspartate aminotransferase (aspC)
ORF00596	asparaginyl-tRNA synthetase (asnS)
ORF00601	conserved hypothetical protein
ORF00602	conserved hypothetical protein
ORF00603	conserved hypothetical protein
ORF00605	zinc ABC transporter, zinc-binding adhesion liprotein
ORF00606	ribosomal protein L31 (rpmE)
ORF00607	DHH family protein
ORF00609	flavodoxin
ORF00614	ribosomal protein L19 (rplS)
ORF00640	prophage LambdaSa1, single-strand binding protein (ssb)
ORF00693	DNA-binding response regulator VncR (vncR)
ORF00694	sensor histidine kinase VncS (vncS)
ORF00699	rod shape-determining protein RodA, putative□ (rodA)
ORF00700	hydrolase, haloacid dehalogenase-like family
ORF00701	DNA gyrase, B subunit (gyrB)
ORF00702	septation ring formation regulator EzrA, putative
ORF00705	conserved hypothetical protein
ORF00706	enolase (eno)
ORF00708	3-phosphoshikimate 1-carboxyvinyltransferase (aroA)
ORF00709	shikimate kinase (aroK)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation
ORF00710 psr protein
ORF00711 RNA methyltransferase, TrmA family
ORF00729 sortase family protein
ORF00731 sortase family protein
ORF00734 sortase family protein, FRAMESHIFT
ORF00743 ABC transporter, ATP-binding protein
ORF00744 membrane protein
ORF00745 conserved hypothetical protein
ORF00748 cylG protein (cylG)
ORF00776 DNA-entry nuclease, putative
ORF00789 2-keto-3-deoxygluconate kinase
ORF00792 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase (eda)
ORF00798 proline dipeptidase (pepQ)
ORF00799 transcriptional regulator, RegM family
ORF00802 glycosyl transferase, group 1 family protein
ORF00803 threonyl-tRNA synthetase (thrS)
ORF00804 DNA-binding response regulator
ORF00808 amino acid ABC transporter, permease protein
ORF00810 amino acid ABC transporter, ATP-binding protein
ORF00811 DNA-binding response regulator
ORF00812 sensory box histidine kinase
ORF00813 metallo-beta-lactamase family protein
ORF00815 ribonuclease III (rnc)
ORF00816 expressed putative chromosome segregation SMC protein
ORF00817 hydrolase, haloacid dehalogenase-like family
ORF00818 hydrolase, haloacid dehalogenase-like family
ORF00819 signal recognition particle-docking protein FtsY (ftsY)
ORF00820 ABC transporter, substrate-binding protein
ORF00821 ABC transporter, permease protein, putative
ORF00824 transcriptional accessory protein Tex, putative
ORF00825 conserved hypothetical protein
ORF00828 HPr(Ser) kinase/phosphatase (hprK)
ORF00830 prolipoprotein diacylglyceryl transferase (lgt)
ORF00832 conserved hypothetical protein
ORF00835 peptidase, U32 family, putative
ORF00836 peptidase, U32 family
ORF00837 conserved hypothetical protein
ORF00844 lysyl-tRNA synthetase (lysS)
ORF00846 phosphoglycerate mutase family protein
ORF00847 ebsC family protein, putative
ORF00850 peptidase, U32 family
ORF00855 oligoendopeptidase F, putative
ORF00856 phosphoenolpyruvate carboxylase (ppc)
ORF00859 cell division protein, FtsW/RodA/SpoVE family (ftsW)
ORF00861 translation elongation factor Tu (tuf)
ORF00863 triosephosphate isomerase (tpiA)
ORF00865 phosphoglycerate mutase (gpmA)
ORF00867 recombination protein RecR (recR)
ORF00868 D-alanine--D-alanine ligase
ORF00869 UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase (murF)
ORF00870 oxalate:formate antiporter
ORF00871 membrane protein, putative
ORF00873 peptide chain release factor 3 (prfC)
ORF00876 ABC transporter, ATP-binding protein
ORF00880 ATP-dependent RNA helicase, DEAD/DEAH box family

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx	Annotation
ORF00882	conserved hypothetical protein
ORF00883	conserved hypothetical protein
ORF00884	acyltransferase family protein
ORF00885	competence protein CelA (celA)
ORF00887	DNA internalization-related competence protein ComEC/Rec2
ORF00889	sugar-binding transcriptional regulator, LacI family
ORF00892	DNA polymerase III, delta subunit, putative□
ORF00893	superoxide dismutase, Fe-Mn (sodA)
ORF00894	transcriptional antiterminator LicT
ORF00895	PTS system, beta-glucosides-specific IIABC components
ORF00896	6-phospho-beta-glucosidase (bglA)
ORF00899	glycerate kinase 2 (garK)
ORF00904	S-adenosylmethionine:tRNA ribosyltransferase-isomerase (queA)
ORF00906	glucosamine-6-phosphate isomerase (nagB)
ORF00908	ribosomal small subunit pseudouridine synthase
ORF00911	competence protein CoiA (coiA)
ORF00912	oligoendopeptidase B (pepB)
ORF00914	O-methyltransferase family protein
ORF00916	protease maturation protein, putative
ORF00919	alanyl-tRNA synthetase (alaS)
ORF00925	transcriptional regulator, Cro/CI family
ORF00928	ribonucleoside-diphosphate reductase 2, beta subunit (nrdF)
ORF00929	ribonucleoside-diphosphate reductase 2, alpha subunit (nrdE)
ORF00930	ribonucleoside-diphosphate reductase 2, NrdH-redoxin (nrdH)
ORF00931	phosphocarrier protein HPr (ptsH)
ORF00932	phosphoenolpyruvate-protein phosphotransferase (ptsI)
ORF00933	glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent (gapN)
ORF00934	polysaccharide deacetylase family protein
ORF00935	ATP-dependent RNA helicase, DEAD/DEAH box family
ORF00936	uridine kinase (udk)
ORF00937	conserved hypothetical protein
ORF00938	DNA polymerase III, gamma and tau subunits (dnaX)
ORF00940	biotin--acetyl-CoA-carboxylase ligase
ORF00941	S-adenosylmethionine synthetase (metK)
ORF00955	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (murA)
ORF00956	acetyltransferase, GNAT family
ORF00957	CBS domain protein
ORF00958	methionine aminopeptidase, type I (map)
ORF00959	ribonuclease BN, putative
ORF00962	conserved hypothetical protein
ORF00963	DNA ligase, NAD-dependent (ligA)
ORF00964	BmrU protein, putative
ORF00966	pullulanase, putative
ORF00973	ATP synthase F0, A subunit (atpB)
ORF00974	ATP synthase F0, B subunit (atpF)
ORF00975	ATP synthase F1, delta subunit (atpH)
ORF00976	ATP synthase F1, alpha subunit (atpA)
ORF00977	ATP synthase F1, gamma subunit (atpG)
ORF00978	ATP synthase F1, beta subunit (atpD)
ORF00979	ATP synthase F1, epsilon subunit (atpC)
ORF00981	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (murA)
ORF00983	DNA-entry nuclease (endA)
ORF00984	phenylalanyl-tRNA synthetase, alpha subunit (pheS)
ORF00986	phenylalanyl-tRNA synthetase, beta subunit (pheT)
ORF00988	exonuclease RexB (rexB)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx	Annotation
ORF00989	exonuclease RexA (rexA)
ORF00991	tRNA modification GTPase TrmE (trmE)
ORF00992	ABC transporter, ATP-binding protein
ORF00993	acetoin dehydrogenase, thymine PPi dependent, E1 component, alpha subunit
ORF00994	acetoin dehydrogenase, thymine PPi dependent, E1 component, beta subunit
ORF00995	acetoin dehydrogenase, thymine PPi dependent, E2 component, dihydrolipoamide
ORF00996	acetoin dehydrogenase, thymine PPi dependent, E3 component, dihydrolipoamide dehydrogenase
ORF00997	lipoate-protein ligase A (lplA)
ORF00998	cobyric acid synthase, putative
ORF00999	mur ligase family protein
ORF01000	conserved hypothetical protein TIGR00159
ORF01001	expressed protein of unknown function
ORF01002	phosphoglucomutase/phosphomannomutase family protein
ORF01005	oxygen-independent coproporphyrinogen III oxidase, putative
ORF01006	conserved hypothetical protein
ORF01007	hydrolase, haloacid dehalogenase-like family
ORF01008	conserved hypothetical protein
ORF01023	GTP-binding protein LepA (lepA)
ORF01027	PilB-related protein
ORF01030	cation-transporting ATPase, E1-E2 family
ORF01033	conserved hypothetical protein
ORF01040	Tn916, tetracycline resistance protein (tetM)
ORF01057	transcriptional regulator, GntR family
ORF01058	DNA polymerase III, alpha subunit (dnaE)
ORF01059	6-phosphofructokinase (pfk)
ORF01060	pyruvate kinase (pyk)
ORF01063	glucosamine--fructose-6-phosphate aminotransferase (isomerizing) (glmS)
ORF01066	phnA protein (phnA)
ORF01068	amino acid ABC transporter, permease protein
ORF01069	amino acid ABC transporter, ATP-binding protein
ORF01070	amino acid ABC transporter, amino acid-binding protein
ORF01072	ribosomal protein S20 (rpsT)
ORF01073	pantothenate kinase (coaA)
ORF01074	conserved hypothetical protein
ORF01075	cytidine deaminase (cdd)
ORF01076	expressed putative lipoprotein
ORF01077	sugar ABC transporter, ATP-binding protein
ORF01078	sugar ABC transporter, permease protein, putative
ORF01079	sugar ABC transporter, permease protein, putative
ORF01080	NADH oxidase (nox-2)
ORF01081	L-lactate dehydrogenase (ldh)
ORF01082	DNA gyrase, A subunit (gyrA)
ORF01083	sortase SrtA (srtA)
ORF01089	GMP synthase (guaA)
ORF01090	transcriptional regulator, GntR family
ORF01091	gid protein (gid)
ORF01093	expressed putative lipoprotein
ORF01097	ABC transporter, ATP-binding protein
ORF01099	DNA-binding response regulator
ORF01101	site-specific recombinase, phage integrase family
ORF01106	signal recognition particle protein Ffh (ffh)
ORF01108	conserved hypothetical protein
ORF01109	sensor histidine kinase CiaH
ORF01110	DNA-binding response regulator CiaR (ciaR)
ORF01111	aminopeptidase N (pepN)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx	Annotation
ORF01112	phosphate transport system regulatory protein PhoU (phoU)
ORF01113	phosphate ABC transporter, ATP-binding protein PstB, putative
ORF01114	phosphate ABC transporter, ATP-binding protein PstB, putative
ORF01115	phosphate ABC transporter, permease protein PstA, putative
ORF01116	phosphate ABC transporter, permease protein
ORF01117	phosphate ABC transporter, phosphate-binding protein
ORF01118	NOL1/NOP2/sun family protein
ORF01119	inositol monophosphatase family protein
ORF01120	conserved hypothetical protein
ORF01121	conserved hypothetical protein
ORF01122	macrolide-efflux protein mreA/riboflavin biosynthesis protein RibF
ORF01123	tRNA pseudouridine synthase B (truB)
ORF01125	conserved hypothetical protein
ORF01128	permease, putative
ORF01129	ABC transporter, ATP-binding protein
ORF01131	DNA topoisomerase I (topA)
ORF01132	DprA/SMF protein, putative DNA processing factor (dprA)
ORF01134	iron compound ABC transporter, ATP-binding protein
ORF01137	acetyltransferase, CysE/LacA/LpxA/NodL family
ORF01138	ribonuclease HII (rnhB)
ORF01139	GTP-binding protein
ORF01176	carbamoyl-phosphate synthase, large subunit (carB)
ORF01177	carbamoyl-phosphate synthase, small subunit (carA)
ORF01178	aspartate carbamoyltransferase (pyrB)
ORF01179	dihydroorotase, multifunctional complex type (pyrC)
ORF01180	orotate phosphoribosyltransferase (pyrE)
ORF01181	orotidine 5'-phosphate decarboxylase (pyrF)
ORF01183	ABC transporter, ATP-binding protein
ORF01184	ribonucleotide reductase, truncation
ORF01188	cardiolipin synthetase (cls)
ORF01189	formate--tetrahydrofolate ligase (fhs)
ORF01190	lipoate-protein ligase A (lplA)
ORF01198	flavoprotein-related protein
ORF01199	flavoprotein family protein
ORF01200	membrane protein, putative
ORF01201	phosphoglucomutase (pgm)
ORF01203	IS861, transposase OrfB
ORF01205	ABC transporter, ATP-binding/permease protein
ORF01206	ABC transporter, ATP-binding/permease protein
ORF01207	conserved hypothetical protein
ORF01208	conserved hypothetical protein
ORF01209	Serine hydroxymethyltransferase
ORF01210	Sua5/YciO/YrdC/YwlC family protein
ORF01211	modification methylase, HemK family
ORF01212	peptide chain release factor 1 (prfA)
ORF01213	thymidine kinases (tdk)
ORF01214	4-oxalocrotonate tautomerase (xylM)
ORF01216	ApbE family protein
ORF01220	xanthine permease (pbuX)
ORF01221	xanthine phosphoribosyltransferase (xpt)
ORF01222	guanosine monophosphate reductase (guaC)
ORF01227	phosphate acetyltransferase
ORF01228	ribosomal large subunit pseudouridine synthase, RluD subfamily
ORF01229	expressed protein of unknown function
ORF01230	GTP pyrophosphokinase family protein

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx	Annotation
ORF01231	conserved hypothetical protein
ORF01232	ribose-phosphate pyrophosphokinase (prsA)
ORF01233	cysteine desulphurase (iscS)
ORF01234	conserved hypothetical protein
ORF01235	conserved hypothetical protein
ORF01236	DNA repair protein RadC (radC)
ORF01238	6-phospho-beta-glucosidase (ascB)
ORF01239	platelet activating factor, putative
ORF01240	hydrolase, haloacid dehalogenase-like family
ORF01242	voltage-gated chloride channel family protein
ORF01243	spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein (potD)
ORF01244	spermidine/putrescine ABC transporter, permease protein (potC)
ORF01245	spermidine/putrescine ABC transporter, permease protein (potB)
ORF01246	spermidine/putrescine ABC transporter, ATP-binding protein (potA)
ORF01247	UDP-N-acetylenolpyruvoylglucosamine reductase (murB)
ORF01248	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase (folK)
ORF01250	dihydropteroate synthase (folP)
ORF01251	GTP cyclohydrolase I (folE)
ORF01252	folylpolyglutamate synthase (folC)
ORF01259	aldehyde dehydrogenase family protein
ORF01260	membrane protein
ORF01274	gls24 protein, putative
ORF01276	gls24 protein, putative
ORF01279	conserved hypothetical protein
ORF01282	ATP-dependent DNA helicase PcrA (pcrA)
ORF01283	conserved hypothetical protein, FRAMESHIFT
ORF01284	uracil permease (uraA)
ORF01285	sodium:alanine symporter family protein
ORF01286	cation efflux family protein
ORF01290	ribosomal protein S1 (rpsA)
ORF01292	branched-chain amino acid aminotransferase (ilvE)
ORF01294	DNA topoisomerase IV, A subunit (parC)
ORF01295	DNA topoisomerase IV, B subunit (parE)
ORF01296	membrane protein, putative
ORF01297	uracil-DNA glycosylase (ung)
ORF01317	transcriptional regulator, LysR family, putative
ORF01319	purine nucleoside phosphorylase (deoD)
ORF01321	purine nucleoside phosphorylase (deoD)
ORF01323	phosphopentomutase (deoB)
ORF01324	ribose 5-phosphate isomerase (rpiA)
ORF01327	tributyrin esterase (estA)
ORF01328	metallo-beta-lactamase superfamily protein
ORF01329	ABC transporter, ATP-binding protein
ORF01330	ABC transporter, permease protein
ORF01331	conserved hypothetical protein
ORF01332	adherence and virulence protein A (pavA)
ORF01335	TPR domain protein
ORF01336	membrane protein
ORF01338	mutator MutT protein (mutX)
ORF01339	hyaluronidase
ORF01343	iminodiacetate oxidase, putative
ORF01344	conserved hypothetical protein TIGR00486
ORF01345	**conserved hypothetical protein**
ORF01346	DNA replication protein Dnad, putative
ORF01347	adenine phosphoribosyltransferase (apt)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx	Annotation
ORF01350	single-stranded-DNA-specific exonuclease RecJ (recJ)
ORF01351	oxidoreductase, short chain dehydrogenase/reductase family
ORF01352	metallo-beta-lactamase superfamily protein
ORF01353	conserved hypothetical protein
ORF01354	GTP-binding protein HflX (hflX)
ORF01355	tRNA delta(2)-isopentenylpyrophosphate transferase (miaA)
ORF01357	exfoliative toxin A, putative
ORF01358	pullulanase, putative
ORF01362	conserved hypothetical protein
ORF01363	peptidase, M20/M25/M40 family
ORF01364	nitroreductase family protein
ORF01367	excinuclease ABC, C subunit (uvrC)
ORF01380	streptococcal histidine triad family protein
ORF01381	laminin-binding surface protein (lmb)
ORF01397	Tn5252, relaxase
ORF01403	mercuric reductase (merA)
ORF01406	IS861, transposase OrfB, truncation
ORF01407	cation-transporting ATPase, E1-E2 family
ORF01411	conserved hypothetical protein
ORF01412	cation-transporting ATPase, E1-E2 family
ORF01415	transcriptional repressor CopY, putative
ORF01416	cadmium resistance transporter, putative
ORF01451	C-5 cytosine-specific DNA methylase
ORF01453	conserved hypothetical protein
ORF01455	ribosomal protein L7/L12 (rplL)
ORF01456	ribosomal protein L10 (rplJ)
ORF01458	ATP-dependent Clp protease, ATP-binding subunit
ORF01467	GTP-binding protein (cgpA)
ORF01468	ATP-dependent Clp protease, ATP-binding subunit ClpX (clpX)
ORF01470	dihydrofolate reductase (folA)
ORF01471	thymidylate synthase (thyA)
ORF01472	HMG-CoA synthase
ORF01473	3-hydroxy-3-methylglutaryl-CoA reductase
ORF01474	conserved hypothetical protein
ORF01475	hemolysin III, putative
ORF01476	conserved hypothetical protein TIGR00147
ORF01479	isopentenyl-diphosphate delta-isomerase
ORF01480	phosphomevalonate kinase
ORF01481	diphosphomevalonate decarboxylase (mvaD)
ORF01482	mevalonate kinase, putative
ORF01484	DNA-binding response regulator
ORF01491	polypeptide deformylase, putative
ORF01495	ABC transporter, ATP-binding/permease protein
ORF01496	ABC transporter, ATP-binding/permease protein
ORF01498	ABC transporter, ATP-binding protein
ORF01499	polyA polymerase family protein
ORF01500	DegV family protein
ORF01501	expressed protein of unknown function
ORF01504	PTS system, fructose specific IIABC components
ORF01505	1-phosphofructokinase (fruK)
ORF01506	lactose phosphotransferase system repressor (lacR)
ORF01507	beta-lactam resistance factor
ORF01511	pyridine nucleotide-disulphide oxidoreductase family protein
ORF01512	tRNA (guanine-N1)-methyltransferase (trmD)
ORF01513	16S rRNA processing protein RimM (rimM)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx	Annotation
ORF01515	transcriptional regulator, RofA family
ORF01516	KH domain protein
ORF01517	ribosomal protein S16 (rpsP)
ORF01518	permease, putative
ORF01519	ABC transporter, ATP-binding protein
ORF01520	conserved hypothetical protein
ORF01523	carbamoyl-phosphate synthase, small subunit (carA)
ORF01524	pyrimidine operon regulatory protein (pyrR)
ORF01525	ribosomal large subunit pseudouridine synthase, RluD subfamily
ORF01526	lipoprotein signal peptidase (lspA)
ORF01527	transcriptional regulator, LysR family
ORF01528	ribosomal protein L27 (rpmA)
ORF01529	conserved hypothetical protein
ORF01530	ribosomal protein L21 (rplU)
ORF01531	conserved hypothetical protein, FRAMESHIFT
ORF01532	thiamine biosynthesis protein ThiI (thiI)
ORF01533	cysteine desulphurase (iscS)
ORF01536	glutathione reductase (gor)
ORF01537	conserved hypothetical protein
ORF01538	chorismate synthase (aroC)
ORF01539	3-dehydroquinate synthase (aroB)
ORF01540	3-dehydroquinate dehydratase (aroD)
ORF01541	conserved hypothetical protein
ORF01543	ribosomal protein L20 (rplT)
ORF01544	ribosomal protein L35 (rpmI)
ORF01545	translation initiation factor IF-3 (infC)
ORF01546	cytidylate kinase (cmk)
ORF01548	ferredoxin, 4Fe-4S
ORF01550	peptidase t (pepT)
ORF01551	polysaccharide biosynthesis protein, putative
ORF01552	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (murE)
ORF01553	iron compound ABC transporter, ATP-binding protein (fepC)
ORF01555	iron compound ABC transporter, permease protein
ORF01556	iron compound ABC transporter, permease protein
ORF01558	inorganic pyrophosphatase, manganese-dependent (ppa)
ORF01559	pyruvate formate-lyase-activating enzyme (pflA)
ORF01560	CBS domain protein
ORF01561	conserved hypothetical protein
ORF01564	PAP2 family protein
ORF01565	membrane protein, putative
ORF01567	expressed sortase family protein
ORF01568	sortase family protein
ORF01571	rogB protein FRAMESHIFT (rogB)
ORF01587	conserved hypothetical protein
ORF01589	RNA polymerase sigma-70 factor (rpoD)
ORF01590	DNA primase (dnaG)
ORF01591	large conductance mechanosensitive channel protein (mscL)
ORF01592	ribosomal protein S21 (rpsU)
ORF01594	amino acid ABC transporter, amino acid-binding protein
ORF01598	rhodanese family protein
ORF01602	glycogen phosphorylase (glgP)
ORF01603	4-alpha-glucanotransferase (malQ)
ORF01604	maltose operon repressor MalR, putative
ORF01605	maltose/maltodextrin ABC transporter, maltose/maltodextrin-binding protein
ORF01606	maltose ABC transporter, permease protein

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation
ORF01607 maltose ABC transporter, permease protein
ORF01614 preprotein translocase SecA subunit, putative
ORF01619 preprotein translocase SecY family protein
ORF01634 excinuclease ABC, B subunit (uvrB)
ORF01636 glutamine ABC transporter, glutamine-binding protein/permease protein (glnP)
ORF01637 glutamine ABC transporter, ATP-binding protein, GlnQ putative
ORF01640 GTP-binding protein, GTP1/Obg family (obg)
ORF01646 amidase family protein
ORF01647 ribosomal small subunit pseudouridine synthase A (rsuA)
ORF01648 oxidoreductase, aldo/keto reductase family
ORF01651 lactoylglutathione lyase (gloA)
ORF01652 glycosyl transferase, group 2 family protein
ORF01654 SsrA-binding protein (smpB)
ORF01655 exoribonuclease, VacB/Rnb family (vacB)
ORF01657 preprotein translocase, SecG subunit
ORF01658 multi-drug resistance protein
ORF01662 dephospho-CoA kinase
ORF01663 formamidopyrimidine-DNA glycosylase (mutM)
ORF01677 GTP-binding protein Era (era)
ORF01678 diacylglycerol kinase (dgkA)
ORF01679 conserved hypothetical protein TIGR00043
ORF01685 PhoH family protein
ORF01687 conserved hypothetical protein
ORF01689 conserved hypothetical protein
ORF01690 ribosome recycling factor (frr)
ORF01691 uridylate kinase (pyrH)
ORF01693 peptide ABC transporter, ATP-binding protein FRAMESHIFT
ORF01697 ribosomal protein L1 (rplA)
ORF01698 ribosomal protein L11 (rplK)
ORF01706 IS861, transposase OrfB
ORF01707 chorismate binding enzyme
ORF01708 FtsK/SpoIIIE family protein
ORF01709 peptidyl-prolyl cis-trans isomerase, cyclophilin-type
ORF01710 manganese ABC transporter, permease protein
ORF01711 manganese ABC transporter, ATP-binding protein
ORF01712 manganese ABC transporter, manganese-binding adhesion liprotein
ORF01713 iron-dependent transcriptional regulator
ORF01714 5-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase (pfs)
ORF01716 MutT/nudix family protein
ORF01718 UDP-N-acetylglucosamine pyrophosphorylase (glmU)
ORF01722 oxidoreductase, Gfo/Idh/MocA family
ORF01725 gluconate 5-dehydrogenase, putative
ORF01726 conserved hypothetical protein
ORF01738 branched-chain amino acid transport system II carrier protein (brnQ)
ORF01739 methionyl-tRNA synthetase (metG)
ORF01745 exodeoxyribonuclease (exoA)
ORF01746 conserved hypothetical protein
ORF01752 copper homeostasis protein CutC, putative
ORF01755 tetrapyrrole methylase family protein
ORF01756 conserved hypothetical protein
ORF01758 DNA polymerase III, delta prime subunit, putative
ORF01759 thymidylate kinase (tmk)
ORF01773 ATP-dependent Clp protease, proteolytic subunit ClpP (clpP)
ORF01774 uracil phosphoribosyltransferase (upp)
ORF01777 RNA methyltransferase, TrmH family, group 2

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx	**Annotation**
ORF01781	conserved hypothetical protein TIGR00278
ORF01782	ribosomal large subunit pseudouridine synthase B (rluB)
ORF01783	conserved hypothetical protein TIGR00281
ORF01784	conserved hypothetical protein
ORF01785	integrase/recombinase, phage integrase family
ORF01786	CBS domain protein
ORF01787	conserved hypothetical protein
ORF01788	HAM1 protein
ORF01789	glutamate racemase (murI)
ORF01791	membrane protein, putative
ORF01792	transcriptional regulator, biotin repressor family
ORF01793	membrane protein, putative
ORF01795	RNA methyltransferase, TrmH family
ORF01796	acylphosphatase
ORF01797	lipoprotein, putative
ORF01799	amino acid ABC transporter, permease protein
ORF01801	amidase family protein
ORF01802	transcription elongation factor GreA (greA)
ORF01803	conserved hypothetical protein
ORF01804	acetyltransferase, GNAT family
ORF01805	UDP-N-acetylmuramate--alanine ligase (murC)
ORF01806	conserved hypothetical protein
ORF01808	expressed putative helicase
ORF01811	phosphoglycerate dehydrogenase-related protein
ORF01812	primosomal protein DnaI (dnaI)
ORF01813	conserved hypothetical protein
ORF01814	conserved hypothetical protein TIGR00244
ORF01815	sensor histidine kinase CsrS (csrS)
ORF01816	DNA-binding response regulator CsrR (csrR)
ORF01817	conserved hypothetical protein
ORF01818	heat shock protein HtpX (htpX)
ORF01820	lemA protein (lemA)
ORF01821	glucose-inhibited division protein B (gidB)
ORF01822	sodium transport family protein
ORF01823	potassium uptake protein, Trk family, putative
ORF01825	ABC transporter, ATP-binding protein
ORF01828	branched-chain amino acid transport system II carrier protein (brnQ)
ORF01829	alcohol dehydrogenase, zinc-containing (adh)
ORF01830	ABC transporter, permease protein
ORF01831	ABC transporter, ATP-binding protein
ORF01833	expressed YaeC family protein
ORF01834	ABC transporter, substrate-binding protein
ORF01835	glutamine amidotransferase, class I
ORF01837	conserved hypothetical protein TIGR01033
ORF01846	glycerol uptake facilitator protein (glpF)
ORF01849	conserved hypothetical protein
ORF01851	conserved hypothetical protein
ORF01852	iojap-related protein
ORF01854	conserved hypothetical protein TIGR00488
ORF01855	conserved hypothetical protein TIGR00482
ORF01856	conserved hypothetical protein TIGR00253
ORF01857	GTP-binding protein
ORF01858	**hydrolase, haloacid dehalogenase-like family**
ORF01860	glutamyl-tRNA(Gln) amidotransferase, B subunit (gatB)
ORF01861	glutamyl-tRNA(Gln) amidotransferase, A subunit (gatA)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx	Annotation
ORF01862	glutamyl-tRNA(Gln) amidotransferase, C subunit (gatC)
ORF01867	isochorismatase family protein
ORF01869	transcriptional regulator CodY, putative
ORF01870	aminotransferase, class I
ORF01871	universal stress protein family FRAMESHIFT
ORF01872	hydrolase, haloacid dehalogenase-like family
ORF01873	asparaginase family protein
ORF01874	shikimate 5-dehydrogenase (aroE)
ORF01876	ATP-dependent DNA helicase RecG (recG)
ORF01878	alanine racemase (alr)
ORF01879	holo-(acyl-carrier-protein) synthase (acpS)
ORF01881	preprotein translocase, SecA subunit (secA)
ORF01882	mannose-6-phosphate isomerase, class I (manA)
ORF01883	fructokinase (scrK)
ORF01885	PTS system IIABC components
ORF01886	sucrose-6-phosphate hydrolase (scrB)
ORF01887	sucrose operon repressor ScrR (scrR)
ORF01888	N utilization substance protein B (nusB)
ORF01889	conserved hypothetical protein
ORF01890	translation elongation factor P (efp)
ORF01900	cytidine/deoxycytidylate deaminase family protein
ORF01906	excinuclease ABC, A subunit (uvrA)
ORF01907	conserved hypothetical protein
ORF01908	magnesium transporter, CorA family (corA)
ORF01909	ribosomal protein S18 (rpsR)
ORF01910	single-strand binding protein (ssb)
ORF01911	ribosomal protein S6 (rpsF)
ORF01912	A/G-specific adenine glycosylase (mutY)
ORF01914	thioredoxin (trx)
ORF01915	PAP2 family protein
ORF01916	MutS2 family protein
ORF01917	conserved hypothetical protein
ORF01918	conserved hypothetical protein
ORF01919	ribonuclease HIII (rnhC)
ORF01920	signal peptidase I
ORF01921	helicase, putative
ORF01923	DNA-damage inducible protein P (dinP)
ORF01924	formate acetyltransferase (pflD)
ORF01926	conserved hypothetical protein
ORF01927	proteinase, putative, degenerate, FRAMESHIFT
ORF01929	glycerol uptake facilitator protein, putative
ORF01930	universal stress protein family
ORF01933	X-pro dipeptidyl-peptidase (pepX)
ORF01937	ABC transporter, ATP-binding protein CydC (cydC)
ORF01938	ABC transporter, ATP-binding protein CydD
ORF01945	conserved hypothetical protein TIGR00103
ORF01948	exonuclease
ORF01949	conserved hypothetical protein
ORF01950	conserved hypothetical protein TIGR00275
ORF01952	ribosomal protein S14 (rpsN)
ORF01957	O-sialoglycoprotein endopeptidase family protein
ORF01958	ribosomal-protein-alanine acetyltransferase, putative
ORF01960	expressed protein of unknown function
ORF01961	conserved hypothetical protein
ORF01962	metallo-beta-lactamase superfamily protein

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation
ORF01963 conserved hypothetical protein
ORF01964 glutamine synthetase, type I (glnA)
ORF01965 transcriptional regulator GlnR (glnR)
ORF01967 conserved hypothetical protein
ORF01969 phosphoglycerate kinase (pgk)
ORF01971 glyceraldehyde 3-phosphate dehydrogenase (gap)
ORF01972 translation elongation factor G (fusA)
ORF01973 ribosomal protein S7 (rpsG)
ORF01974 ribosomal protein S12 (rpsL)
ORF01975 pur operon repressor (purR)
ORF01976 HD domain protein
ORF01977 conserved hypothetical protein
ORF01978 conserved hypothetical protein
ORF01979 ribulose-phosphate 3-epimerase (rpe)
ORF01980 conserved hypothetical protein TIGR00157
ORF01983 dimethyladenosine transferase (ksgA)
ORF01985 primase-related protein
ORF01987 deoxyribonuclease, TatD family
ORF01992 dltD protein (dltD)
ORF01993 D-alanyl carrier protein (dltC)
ORF01994 dltB protein (dltB)
ORF01996 D-alanine-activating enzyme (dltA)
ORF01997 sensor histidine kinase
ORF01998 DNA-binding response regulator
ORF01999 ribosomal protein L34 (rpmH)
ORF02004 amino acid ABC transporter, ATP-binding protein
ORF02007 conserved hypothetical protein
ORF02008 transcriptional antiterminator, BglG family
ORF02017 sugar binding transcriptional regulator, LacI family
ORF02018 transaldolase family protein
ORF02019 carbohydrate isomerase, AraD/FucA family
ORF02020 hexulose-6-phosphate isomerase, putative
ORF02021 hexulose-6-phosphate synthase, putative
ORF02022 PTS system, IIA component
ORF02023 PTS system, IIB component
ORF02024 transport protein SgaT, putative
ORF02027 adenylosuccinate synthetase (purA)
ORF02033 chaperonin, 33 kDa (hslO)
ORF02034 NifR3/Smm1 family protein
ORF02037 ATP-dependent Clp protease, ATP-binding subunit
ORF02038 transcriptional regulator CtsR (ctsR)
ORF02040 translation elongation factor Ts (tsf)
ORF02041 ribosomal protein S2 (rpsB)
ORF02043 alkyl hydroperoxide reductase, subunit F (ahpF)
ORF02076 prophage LambdaSa2, single-strand binding protein (ssb)
ORF02082 prophage LambdaSa2, type II DNA modification methyltransferase, putative
ORF02086 prophage LambdaSa2, replicative DNA helicase (dnaC)
ORF02104 endopeptidase O (pepO)
ORF02110 polypeptide deformylase (def)
ORF02111 sugar binding transcriptional regulator RegR (regR)
ORF02112 conserved hypothetical protein
ORF02113 PTS system, IID component
ORF02114 PTS system, IIC component
ORF02115 PTS system, IIB component
ORF02116 glucuronyl hydrolase

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation
ORF02118 PTS system, IIA component
ORF02120 oxidoreductase, short-chain dehydrogenase/reductase family
ORF02121 conserved hypothetical protein
ORF02122 carbohydrate kinase, PfkB family
ORF02123 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase (eda)
ORF02127 DNA polymerase III, alpha subunit, Gram-positive type
ORF02129 prolyl-tRNA synthetase (proS)
ORF02130 membrane-associated zinc metalloprotease, putative
ORF02131 phosphatidate cytidylyltransferase (cdsA)
ORF02132 undecaprenyl diphosphate synthase (uppS)
ORF02133 preprotein translocase, YajC subunit (yajC)
ORF02140 glucan 1,6-alpha-glucosidase (dexB)
ORF02141 sugar ABC transporter, ATP-binding protein (msmK)
ORF02142 helix-turn-helix domain protein, fis-type
ORF02144 tagatose 1,6-diphosphate aldolase (lacD)
ORF02145 tagatose-6-phosphate kinase (lacC)
ORF02146 galactose-6-phosphate isomerase, LacB subunit (lacB)
ORF02147 galactose-6-phosphate isomerase, LacA subunit (lacA)
ORF02149 PTS system, IIC component, putative
ORF02150 PTS system, IIB component, putative
ORF02152 PTS system, IIA component, putative
ORF02153 lactose phosphotransferase system repressor (lacR)
ORF02157 adhesion lipoprotein
ORF02158 expressed protein of unknown function TIGR00256
ORF02159 GTP pyrophosphokinase (relA)
ORF02161 nrdI protein (nrdI)
ORF02164 iron ABC transporter, iron-binding protein
ORF02165 DNA-binding response regulator
ORF02167 PTS system, IID component
ORF02168 PTS system, IIC component
ORF02174 ABC transporter, ATP-binding protein
ORF02176 response regulator
ORF02177 conserved hypothetical protein
ORF02178 PTS system, IIABC components
ORF02179 sensor histidine kinase
ORF02180 phosphate regulon response regulator PhoB (phoB)
ORF02182 phosphate ABC transporter, ATP-binding protein (pstB)
ORF02183 phosphate ABC transporter, permease protein
ORF02184 phosphate ABC transporter, permease protein
ORF02188 conserved hypothetical protein TIGR00046
ORF02189 ribosomal protein L11 methyltransferase (prmA)
ORF02197 conserved hypothetical protein
ORF02199 ATPase, AAA family
ORF02249 mercuric reductase (merA)
ORF02272 DNA topology modulation protein FlaR, putative
ORF02273 glycerol dehydrogenase, putative
ORF02281 DNA-binding response regulator
ORF02285 leucyl-tRNA synthetase (leuS)
ORF02290 transcription antitermination protein NusG (nusG)
ORF02293 penicillin-binding protein 2A (pbp2A)
ORF02294 ribosomal large subunit pseudouridine synthase, RluD subfamily
ORF02296 phosphopentomutase (deoB)
ORF02297 deoxyribose-phosphate aldolase (deoC)
ORF02300 uridine phosphorylase (udp)
ORF02302 60 kda chaperonin (groEL)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation
ORF02303 chaperonin, 10 kDa (groES)
ORF02305 ABC transporter, ATP-binding protein
ORF02306 ABC transporter, permease protein
ORF02307 expressed putative lipoprotein
ORF02309 glyoxalase family protein
ORF02310 conserved hypothetical protein
ORF02311 anaerobic ribonucleoside-triphosphate reductase activating protein (nrdG)
ORF02312 acetyltransferase, GNAT family
ORF02315 anaerobic ribonucleoside-triphosphate reductase (nrdD)
ORF02318 conserved hypothetical protein
ORF02320 conserved hypothetical protein
ORF02321 conserved hypothetical protein
ORF02322 recA protein (recA)
ORF02325 DNA-3-methyladenine glycosylase I (tag)
ORF02327 Holliday junction DNA helicase RuvA (ruvA)
ORF02329 DNA mismatch repair protein HexB (hexB)
ORF02333 arginine repressor ArgR, putative
ORF02334 arginyl-tRNA synthetase (argS)
ORF02337 conserved hypothetical protein
ORF02338 conserved hypothetical protein
ORF02339 aspartyl-tRNA synthetase (aspS)
ORF02340 histidyl-tRNA synthetase (hisS)
ORF02342 ribosomal protein L33 (rpmG)
ORF02357 DNA-binding response regulator
ORF02359 membrane protein, putative
ORF02360 carbamate kinase (arcC)
ORF02361 ornithine carbamoyltransferase (argF)
ORF02364 amino acid ABC transporter, ATP-binding protein
ORF02365 amino acid ABC transporter, permease and amino acid-binding protein
ORF02370 membrane protein, putative
ORF02371 transcriptional regulator, TetR family, putative
ORF02373 ribosomal protein S4 (rpsD)
ORF02374 conserved hypothetical protein
ORF02375 replicative DNA helicase (dnaC)
ORF02376 ribosomal protein L9 (rplI)
ORF02377 DHH family protein
ORF02378 glucose inhibited division protein A (gidA)
ORF02380 tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (trmU)
ORF02381 L-serine dehydratase, iron-sulfur-dependent, beta subunit (sdhB)
ORF02382 L-serine dehydratase, iron-sulfur-dependent, alpha subunit (sdhA)
ORF02385 cobalt transport family protein
ORF02386 ABC transporter, ATP-binding protein
ORF02387 ABC transporter, ATP-binding protein, FRAMESHIFT
ORF02388 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (pgsA)
ORF02389 peptidase, M16 family
ORF02390 conserved hypothetical protein
ORF02391 conserved hypothetical protein
ORF02392 recF protein (recF)
ORF02396 inosine-5'-monophosphate dehydrogenase (guaB)
ORF02397 transcriptional regulator, ArgR family
ORF02400 arginine deiminase (arcA)
ORF02402 ornithine carbamoyltransferase (argF)
ORF02404 carbamate kinase (arcC)
ORF02405 tryptophanyl-tRNA synthetase (trpS)
ORF02407 conserved hypothetical protein

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx	Annotation
ORF02408	ABC transporter, ATP-binding protein
ORF02409	ABC transporter, permease protein, putative
ORF02410	conserved hypothetical protein TIGR00246
ORF02411	serine protease
ORF02412	partitioning protein, ParB family
ORF02413	chromosomal replication initiator protein DnaA (dnaA)
ORF02415	DNA polymerase III, beta subunit (dnaN)
ORF02417	conserved hypothetical protein
ORF02419	conserved hypothetical GTP-binding protein
ORF02420	peptidyl-tRNA hydrolase (pth)
ORF02421	transcription-repair coupling factor (mfd)
ORF02423	S4 domain protein
ORF02424	cell division protein DivIC, putative
ORF02426	expressed protein of unknown function
ORF02427	MesJ/Ycf62 family protein
ORF02429	cell division protein FtsH (ftsH)

Table 9: GBS genes shared with pneumococcus

ORFxxxxx	Annotation
ORF00017	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase (purH)
ORF00025	conserved hypothetical protein
ORF00029	acetyl xylan esterase, putative
ORF00042	aldehyde-alcohol dehydrogenase (adhE)
ORF00044	threonine synthase (thrC)
ORF00081	ribosomal protein L17 (rplQ)
ORF00090	conserved hypothetical protein
ORF00129	argininosuccinate synthase (argG)
ORF00156	oligopeptide ABC transporter, substrate-binding protein, putative
ORF00189	protease, putative
ORF00194	thioredoxin family protein
ORF00195	tRNA binding domain protein
ORF00217	conserved domain protein
ORF00218	PTS system, IIB component, putative
ORF00220	transketolase, N-terminal subunit
ORF00221	transketolase, C-terminal subunit
ORF00223	oxidoreductase, putative
ORF00282	acetyltransferase, GNAT family
ORF00290	IS1381, transposase OrfB
ORF00291	IS1381, transposase OrfA
ORF00293	conserved hypothetical protein
ORF00301	membrane protein, putative
ORF00343	ABC transporter, permease protein, putative
ORF00344	conserved hypothetical protein
ORF00382	aspartate kinase family protein
ORF00399	conserved hypothetical protein
ORF00439	cell wall surface anchor family protein
ORF00447	cytidine/deoxycytidylate deaminase family protein
ORF00450	5-formyltetrahydrofolate cyclo-ligase family protein
ORF00480	transcriptional regulator, MerR family
ORF00499	acetyltransferase, GNAT family
ORF00504	magnesium transporter, CorA family
ORF00521	VanZF domain protein
ORF00612	IS1381, transposase OrfA
ORF00613	IS1381, transposase OrfB
ORF00690	transmembrane protein Vexp1 (vex1)
ORF00691	ABC transporter, ATP-binding protein Vexp2 (vex2)
ORF00692	transmembrane protein Vexp3 (vex3)
ORF00714	conserved hypothetical protein
ORF00732	expressed cell wall surface anchor family protein, putative
ORF00774	ABC transporter, ATP-binding protein
ORF00778	ABC transporter, ATP-binding protein
ORF00780	conserved hypothetical protein
ORF00790	beta-glucuronidase
ORF00800	alpha amylase family protein
ORF00807	amino acid ABC transporter, permease protein
ORF00809	amino acid ABC transporter, amino acid-binding protein
ORF00814	conserved hypothetical protein
ORF00823	bacterial luciferase family protein
ORF00840	riboflavin biosynthesis protein RibD (ribD)
ORF00841	riboflavin synthase, alpha subunit (ribE)
ORF00842	riboflavin biosynthesis protein RibA (ribA)
ORF00843	riboflavin synthase, beta subunit (ribH)
ORF00866	penicillin-binding protein 2b
ORF00905	membrane protein, putative

Table 9: GBS genes shared with pneumoccocus

ORFxxxxx Annotation
ORF00910 major facilitator family protein
ORF00913 hydrolase, haloacid dehalogenase-like family
ORF00918 conserved hypothetical protein
ORF00945 conserved hypothetical protein
ORF00948 ABC transporter, ATP-binding protein
ORF00952 phosphomethylpyrimidine kinase (thiD)
ORF00953 hydroxyethylthiazole kinase (thiM)
ORF00954 thiamine-phosphate pyrophosphorylase (thiE)
ORF00961 GtrA family protein
ORF00967 1,4-alpha-glucan branching enzyme (glgB)
ORF00968 glucose-1-phosphate adenylyltransferase (glgC)
ORF00971 glycogen synthase (glgA)
ORF00985 acetyltransferase, GNAT family
ORF00990 magnesium transporter, CorA family, putative
ORF01022 nucleoside diphosphate kinase (ndk)
ORF01031 nucleoside diphosphate kinase domain protein
ORF01085 conserved hypothetical protein
ORF01087 IS1381, transposase OrfA
ORF01088 IS1381, transposase OrfB
ORF01098 ABC transporter, permease protein, putative
ORF01100 sensor histidine kinase
ORF01102 ABC transporter, substrate-binding protein
ORF01127 protease, putative
ORF01135 iron compound ABC transporter, permease protein
ORF01136 iron compound ABC transporter, permease protein
ORF01185 aspartate-semialdehyde dehydrogenase (asd)
ORF01217 conserved hypothetical protein
ORF01218 conserved hypothetical protein
ORF01219 formate/nitrite transporter family protein
ORF01226 oxidoreductase, short chain dehydrogenase/reductase family, FRAMESHIFT
ORF01254 homoserine kinase (thrB)
ORF01255 homoserine dehydrogenase (hom)
ORF01264 transcriptional regulator, Cro/CI family
ORF01268 thiol peroxidase (psaD)
ORF01305 glycosyltransferase CpsJ(V) (cpsJ)
ORF01306 glycosyltransferase CpsO(V) (cpsO)
ORF01313 CpsD protein (cpsD)
ORF01314 cpsC protein (cpsC)
ORF01315 capsular polysaccharide biosynthesis protein CpsB (cpsB)
ORF01316 capsular polysaccharide biosynthesis protein CpsA (cpsA)
ORF01326 conserved hypothetical protein
ORF01333 alpha-acetolactate decarboxylase (budA)
ORF01334 acetolactate synthase, catabolic (ilvK)
ORF01337 MutT/nudix family protein
ORF01369 MATE efflux family protein
ORF01398 Tn5252, Orf 9 protein
ORF01399 Tn5252, Orf 10 protein
ORF01446 protease, putative
ORF01447 conserved hypothetical protein
ORF01449 conserved hypothetical protein
ORF01492 NADP-specific glutamate dehydrogenase (gdhA)
ORF01569 expressed cell wall surface anchor family protein
ORF01570 cell wall surface anchor family protein
ORF01574 polysaccharide biosynthesis protein
ORF01579 nucleotidyl transferase, putative